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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification <sup>5</sup> : C12N 15/11, C12P 21/08 C12Q 1/68, C12N 15/62 C07K 15/28</p>	<p>A2</p>	<p>(11) International Publication Number: <b>WO 94/01548</b>  (43) International Publication Date: 20 January 1994 (20.01.94)</p>
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<p>(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW</p> <p>(57) Abstract</p> <p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>		

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# HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.



A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogenous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

- (a) preparing a mixture comprising a heterogenous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;
- (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;
- (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and
- (d) carrying out an extension synthesis in the mixture produced in step (c).

Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

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Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail-off. Eventually, therefore, all DNA species will be present at the same concentration.

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The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for each DNA population.

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In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

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In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid population is treated by:

- (a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

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(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adapted cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

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(c) selecting and separating only those adapted cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

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A preferred endonuclease for use in step (a) of the above process is Fok I.

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An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

25

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin

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reaction in selecting and separating desired adapted molecules. Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adapted molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

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Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

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and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adapted end of the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adapting" process can be used to generate categories or subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

- (a) a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- (c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that  
5 when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or  
10 sequence in accordance with the invention may be released by the endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

15 Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

20 Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory  
25 sequence.

Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved  
30 using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

35 Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and  
40 Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

- 5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other  
10 methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

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- It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate  
20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate  
25 indication of where the beginnings and ends of the component sequences are.

- In contrast to investigations hitherto, where gene fragments (sequence fragments) could only be identified through some known characteristic  
30 [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by  
35 functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior  
40 art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alession, J. M., et al., Focus (Gibco B.R.L) 9 pl (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltzfuz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher



eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. *Gene* 40 p183 1985), Shimuzu, Y et al., *Gene* 65, p141 (1988), Straus, D. and Gilbert, W. *Proc. Natl. Acad. Sci.* 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. *Nature* 353 pp605-607 (1991), Rudensky, A., Y., et al., *Nature* 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable, although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide. Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase (Nagai, K., and Thogersen, H., *C. Methods Enzymol.* 153 p461-481 (1987)). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

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All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 (1985)).

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#### Example 1

Human-brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age fetuses and then snap frozen in liquid nitrogen before storing in bijou bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA<sup>+</sup> (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983)) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

The column eluate was adjusted to 10 mM  $Mg^{2+}$  and then the purified cDNA was restricted by the action of 1 unit per 10  $\mu$ l of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

The adaptors used were oligonucleotides 5'  $N,N,N,N$ -TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTCGCAGGAGAAGGA (SEQ ID: 1195) and 5'  $AAN,N$ -TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5'  $TTN,N$ -TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added  $MgCl_2$  to 10mM, ATP to 10mM and 0.025 units/ $\mu$ l of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume was 90  $\mu$ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

The column eluate was adjusted to 25mM  $Mg^{2+}$ , 0.5mM dNTPs in a final volume of 200  $\mu$ l. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200  $\mu$ l of streptavidin coated magnetic beads (Dyna) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400µl each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg<sup>2+</sup>. The beads were then resuspended in 240 µl of the  
10 µl.

Four of the 60 µl aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adapted fragments. 2 pmoles of the primer 5' CTGTCTGTCGAGGAGAAGGAA  
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTCGAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes  
20 and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 µl of resuspended beads were added to each reaction to remove the  
25 biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an  
30 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one  
35 of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCACTGTCCGAGAC (SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to  
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8  $\mu$ l or 12.5 % whichever was the larger but not exceeding 12  $\mu$ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM  $Mg^{2+}$ , 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40  $\mu$ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60  $\mu$ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75  $\mu$ l or 75 % of the column eluate, whichever was least, were added 9.5  $\mu$ l of 100mM TrisHCl pH7.4, 100 mM  $MgCl_2$ , and 9.5  $\mu$ l of 0.5 mM dTTP. 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptoring the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACAACCTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptoring were performed according to standard procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C, respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive. In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40µl reactions containing 2.5mM Mg<sup>2+</sup>, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic workstation attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluoroscein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the above procedure.

#### Example 2



A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTGACAAGCTTGAATTCGGGCCGC(T)<sub>26</sub>, (SEQ ID: 1210) was used at 1  $\mu$ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5  $\mu$ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100  $\mu$ l with water.

PCRs were then performed in reactions containing 1  $\mu$ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl<sub>2</sub>, 0.01% gelatin, 200  $\mu$ M dNTPs, 10 uCi a<sup>32</sup>P dCTP, 1  $\mu$ M each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

5

cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyosarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15

Clear plaques from each library were resuspended in 5  $\mu$ l of Tris-HCl pH 8, 1 mM EDTA. 2  $\mu$ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30

Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

35

The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

21

## (1) GENERAL INFORMATION

## (i) APPLICANT

(A) NAME: MEDICAL RESEARCH COUNCIL

5 (B) STREET: 20 PARK CRESCENT

(C) CITY: LONDON

(E) COUNTRY: ENGLAND

(F) POSTAL CODE: WIN 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

## (iv) COMPUTER READABLE FORM:

15

(A) MEDIUM TYPE: DISKETTE

(B) COMPUTER: IBM PC COMPATIBLE

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: EXTRACT

20

## (2) INFORMATION FOR SEQ ID :1:

## (i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCGT GACCAAGAAG GCTCTGTGCA TTCGGGTTTT CCAGGAGACT 50

35 CAAAAGCTGA AGAAGCGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA 100

ATAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTCC AAAGCCATAC 150

CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT 200

40

GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAT ATATCATATA 250

22

TATATATATA CACA

264

## (2) INFORMATION FOR SEQ ID :2:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15 AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT 50  
GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC 100  
CTGGGGAGGG GGTCAATTGTT CTCT 124

20

## (2) INFORMATION FOR SEQ ID :3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC 50  
35 TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC 100  
TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAAACGA ACTGAGATGC 150  
AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA 200  
40 GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA 250

23

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG 300

TCACATATTA GGAAGTATA ACATAAGGTA AAC 333

5 (2) INFORMATION FOR SEQ ID :4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC 50

GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTCT GTCTTTATGT 100

20 AAGAAGAAAC TGCCTAGATG ACGGGGCCCTC CTTCTTCAA CAGGAATTTC 150

TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCC CTGCCCCCAT 200

25 (2) INFORMATION FOR SEQ ID :5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA 50

AGATTTGCCA AATTGTAGCC TACTGGATTC CGGTTCTCTT GACATCTCTT 100

40 TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA 150

24

ATTAAAAAA GGGAGGATT AAGAATAATG AAAAGAGAAA AATCAAGAAA 200

GCACAATCAC TAG 213

5 (2) INFORMATION FOR SEQ ID :6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG 50

GAAGTTTAA GCTAAGATT GCCAAATTGT AGCCTACTGG ATTCCGGTTC 100

20 TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACCTCCC GAGTATAAAC 150

GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG 200

25 AAAAATCAAG AAAGCACAAT CACTAGTGTA GAGATAACAG AATTTCTGAA 250

TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT 300

GTGGCCCATC CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC 345

30

(2) INFORMATION FOR SEQ ID :7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

TCCATTTGAC ATCGCATTTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50  
GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100  
5 GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT 150  
TTCTTTTCC 159

## (2) INFORMATION FOR SEQ ID :8:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20

ATATTTCAAT CGAACAAAAA GGAACTTTT TTTGAACTTA TTGAGGCTCT 50  
ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCCT 100  
25 TGCCTGGCTG GGGGTTTGAT TCGC 124

## (2) INFORMATION FOR SEQ ID :9:

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :9:

CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA 50  
40 TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG 100

26

ACCGGGATGC AGTGTGAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG 150  
GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCCCTGTT 200  
5 CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA 250  
GAAAATAGA 259

## (2) INFORMATION FOR SEQ ID :10:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TCCCCAGGG CCCTCAAGAA 50  
GCTCCTGCAC ACAATAACG CGCCCTCGTT CTTAGCAAG TCTGCTCCCT 100  
25 CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA 150  
GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA 200  
CTGTGACAAG GGGCCC 216

30

## (2) INFORMATION FOR SEQ ID :11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :11:



27

CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG 50  
CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCTGTA 100  
5 AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT 150  
GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG 200  
GGATG 205

10

(2) INFORMATION FOR SEQ ID :12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC 50  
25 AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT 100  
CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA 150  
GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG 200  
30 TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA 250  
TATGCCATTC TCGGTGA 267

35

(2) INFORMATION FOR SEQ ID :13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :13:

5 GCCTCATCAG GTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50  
GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG 100  
CAATGTGAAG CTGAAC 116

## 10 (2) INFORMATION FOR SEQ ID :14:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTGGTCTC TTCGTATGGT CAAACTTCAA 50  
CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG 100  
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT 150  
ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACTCTA 200  
30 AGGGGTGCAA GGACCAGGCT TTGATTTCAA ATTATAATCT AATGCTCACT 250  
CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

## (2) INFORMATION FOR SEQ ID :15:

35

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

29

## (xi) SEQUENCE DESCRIPTION: SEQ ID :15:—

CGTCAGTGTG CTACTTCACA TCATTAGCGA GGCCAGAAA CTTGAACAGG 50  
5 AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC 100  
CAAACTCGAT TCAAAGAGCA ATA 123

## (2) INFORMATION FOR SEQ ID :16:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20

CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT 50  
GGCATTGTCA GAAAAATTTA ACAGGTTTAT TTATAATTAT CATAAAGTTG 100  
25 ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCATTA ATGCTTTACG 150  
TCTCCGCATT TATATTAAAA ATTCACACAC AAATGAAATG GAAAAACTGC 200  
CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA 250  
30 CTTTGTGACTC TA 262

## (2) INFORMATION FOR SEQ ID :17:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :17:

5 TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG 50  
AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT 100  
TGAAAGTAAG TTTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATT 150  
TCAAGAAACG TGCATCAGC 169

10

(2) INFORMATION FOR SEQ ID :18:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :18:

AGGGGCACCA TTACCATCCA TCTGACATCG CATTCCATA GAAATGGCCA 50  
25 AAGAAAGAAG GTCCTGGTAG GTTTTCATA GAAAGACTCA AAAAGTTCAA 100  
CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA 150  
TTATTAAAAT ACTGGCTTCG GTTTCTTTT TTCCTTGCA AAGTTTCCTA 200  
30 CATATATGTC TTTACAGTA T 221

(2) INFORMATION FOR SEQ ID :19:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

31

## (xi) SEQUENCE DESCRIPTION: SEQ ID :19:

TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA 50  
5 TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT 100  
TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC 135

## (2) INFORMATION FOR SEQ ID :20:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20

GTTATCTATC TATCTGCAG TTTACCTATC TGATCTGATC TCTGTAATTA 50  
TAGTTCTGTC ATTTAAATA TACTATTTAA ATCTAATTTT TACATTTCAA 100  
25 AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG 150  
TTATTTTTC AATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT 200  
TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTA AAAAAATTGT 250  
30 ATAATTTTGT GATAATGTAG TTCCCAAAA CACATTTAGA AAGCATTATG 300  
TTATTAGTAA ATGA 314

35

## (2) INFORMATION FOR SEQ ID :21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :21:

5 TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT 50  
TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC 100  
TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT 150  
10 TCCTCTTTCA ATATTTCTGT TTCTTGCC 178

## (2) INFORMATION FOR SEQ ID :22:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :22:

ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT 50  
25 ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA 100  
GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTTT 150  
30 TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT 188

## (2) INFORMATION FOR SEQ ID :23:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

33

## (xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNTCNTTTAN TGCTTTTATA TTTTNAAAT 50  
5 GTTAAAACCC CTATACCACC TTTTGGAAT GTTTAAATT CTCCAATTT 100  
TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTTATCA ATTGAATTGA 150  
GG 152  
10

## (2) INFORMATION FOR SEQ ID :24:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :24:

ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTTCA 50  
25 ACTTTTGAC ACTTTTCAA CGGTCCCACC ACA 83

## (2) INFORMATION FOR SEQ ID :25:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :25:

AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA 50  
40 ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT 100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAC CATNTGCACC 150

CTACATCTGG CTGACATTTA CATTTT 176

5 (2) INFORMATION FOR SEQ ID :26:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACGCTTT TAAATATTT GAACAGAAAA 50

20 GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC 100

TTTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150

TTAAGTACTG ACGAAGAAGA CTAAACAAT CATTTTAA CAATATTAA 200

25 AAGGATCATA TAGTCGACTT TTAACACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG 50

40 GCCCAATCTT CCCAAGTCCA CACAGGAGGG AACATTGTT TGCCTAAATA 100



35

CGCAATGCAA AATTNNNTAT CTTGGCTTAA TACNNGACG TTTTATTTCCG 150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT 100

20 GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 -----T 201

(2) INFORMATION FOR SEQ ID :29:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTTAC TTTATTGGCC 50

40 CCTCCCTACA TTCGGGTTAG GTTCCATTG ATTTGCACAA TAATGACTTT 100

36.

ATTTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTTA TCATAGAACT 150  
AACTATTTTA ATTACATATA ATGTAATAA TGGAGAGATT TATAGAGAAT 200  
5 TTTGTTTTTT TGTATATAC TCCATTTTGA AGACAGATAT GATAGAACTA 250  
GAAATTAAGT TGCATTTCTG CAAGT 275

(2) INFORMATION FOR SEQ ID :30:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20

GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC 50  
ATTCATCAAC AAGATTTCGA ATGGAATATT CCAGAAATTT CTGAGCCATC 100  
25 TGATCACAAC AACCGTCTTT GA 122

(2) INFORMATION FOR SEQ ID :31:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :31:

40

GGATTTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT 50  
AGAGATCTTC CCAATGAACC TCAATACAG ATCGTAATAC TCGCACAATG 100

37

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC 150

TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCAAT GTGAAAC 197

5 (2) INFORMATION FOR SEQ ID :32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG 50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC 97

20

(2) INFORMATION FOR SEQ ID :33:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA 50

35 CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT 100

AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC 150

AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC 200

40

CTAGGAAAAA ATAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT 250

38

CACAATAAGA

260

## (2) INFORMATION FOR SEQ ID :34:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15 GGACNTGCCG NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG 50  
ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT 100  
GATCCAAAAT ACCTTCCTTN CCAAGCCCCG GGTNNNNGAT AAGGTGTGGA 150  
20 NTTNGGTAA AGACAAGG 168

## (2) INFORMATION FOR SEQ ID :35:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35 CTCGNACACT GTGGAGAGCC TGCGNNNNNN NNGGTNTACT CAGGGGGAGG 50  
AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT 100  
GCTNNNGTGG TCCCTTAGNA SCCGAGNAGG TGGGCGCGAG GTGAANAAGG 150  
40 TGCNNGTGCG AGAGTGCGTG ATT 173

39

## (2) INFORMATION FOR SEQ ID :36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :36:

5	AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA	50
15	CAACTAATAA TGATTTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA	100
	GTTTTGCTAA CCTTGGTAAG CTTGTTTACC GTTT	134

20

## (2) INFORMATION FOR SEQ ID :37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :37:

30

30	TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA	50
	ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTGCTC AGTACAGACN	100
35	GATTTACAAT GAAAGTTTTG CTAACCTTGG TAAGCTTGTT AACCGTTTAC	150
	ATGACTTCTT	160

40

## (2) INFORMATION FOR SEQ ID :38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :38:

CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAAATCCCA CCCTCACACG 50  
10 ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT 100  
CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC 140

15

## (2) INFORMATION FOR SEQ ID :39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :39:

AGCAAGTATC ANNNNNNNNN ATACATTGA ATTCAAGTTG TTTTGTGCA 50  
AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG 100  
30 GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG 150  
CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAN NATTANGGGA 200  
35 AAA 203

## (2) INFORMATION FOR SEQ ID :40:

## (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

41

(D)--TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

GAAAAGCNNN NNNNNNNGGC TTAAGAACA ATATGCTGAG ATGGAGAAGG 50  
ACCTAGCGAA ANTNNNAACC TTTAAGAAC TTGAANNACA ACAATCACAA 100  
ACTAATGAGA AGATGTTTAC CTCTCTCTG AAAACTATGC CCACCAGACC 150  
GTTTAGCCTC TGCTCAAGCT 170

15 (2) INFORMATION FOR SEQ ID :41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

GCTGCGTGT TCCTTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA 50  
AAAAGGGAGC CAATAGAGAT CTTCCCAATG AACCTCAAAC ACGTCGTAAT 100  
ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA 150  
CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA 200  
ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG 250  
AAATTTGATT TGTAATAAAA 270

(2) INFORMATION FOR SEQ ID :42:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

42

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :42:

AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC 50  
10 CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT 100  
AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC 150  
15 ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT 200  
GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA 245

## (2) INFORMATION FOR SEQ ID :43:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :43:

30

TAACTGNGA AAATGTACAA AGAAAGTATC CCCRAATNAT TTACAAAGCC 50  
TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA 100  
35 ATGAAGACAC TTTACACTTT TCGG 124

## (2) INFORMATION FOR SEQ ID :44:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



43

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG 50

GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA 100

10

AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA 144

(2) INFORMATION FOR SEQ ID :45:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25 ACTGATTCCNN NNTGAAAATA CCCCTTTTCT CCATTAGTGG CATGCTCATT 50

CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTTTAA 100

CAAAAAAAAA AACACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA 150

30

GAAATTTAAT GTTTTTCATA ACATGAA 177

(2) INFORMATION FOR SEQ ID :46:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

44

(xi) SEQUENCE DESCRIPTION: SEQ ID :46:

ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT 50  
5 TTATCTTTAT ATTCAAATAA GTTATTTGCG TTCACTGTT TTAACAAAAA 100  
AAAAAAAAA AAAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT 150  
TAATTCACAC GGAAAAACCA AGACAATTTC ACAACTTCTG GACACAACCA 200  
10 TCAACACAGG ACATTTTTTT TACAGGCAAA TCACTTAAAA CAAAAAAGAT 250  
CCCAGA 256

15 (2) INFORMATION FOR SEQ ID :47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

GAGAAAAGTC NNNNNNNNA GGTTAATCTA ACTTTTCTTG CTTATTTTCTAG 50  
CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTTTT 100  
30 AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG 150  
AGCAA 155

35 (2) INFORMATION FOR SEQ ID :48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5 GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAATGAT GAATAAGATA 50  
TTNNACAAA GATACACG 68

## (2) INFORMATION FOR SEQ ID :49:

## 10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :49:

20 CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG 50  
GGCCTAGCTA AATTTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA 100  
ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC 150  
25 TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG 200  
AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG 244

## 30 (2) INFORMATION FOR SEQ ID :50:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAAACNCT NNNNCAGAAA 50

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

(2) INFORMATION FOR SEQ ID :51:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15 GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA 50  
AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAT 100  
TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT 150  
20 TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT 200  
TTATACCAGA AGNATGACCA CTG 223

25 (2) INFORMATION FOR SEQ ID :52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTTNT TGTA AAAAAG CTCANNNANA AAGGGANNGG CTTAAGAGA 49

(2) INFORMATION FOR SEQ ID :53:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 base pairs

47

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :53:

CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA	50
TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT	100
TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA	150
TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA	200
TTCAATAATC AAA	213

20

## (2) INFORMATION FOR SEQ ID :54:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :54:

30

GCGTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG	50
CGTNNTTCCG TANGGGGNGG GTTNGGCAG GTGTTGCCGG TAGCNAAACN	100
GTTGGCCCCA TNGCCNGNAT TGNNNCCCN CNNGGGAANG GGGGGGNGA	150
CCNNAGNGGG AAAAAA	166

40

## (2) INFORMATION FOR SEQ ID :55:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :55:

ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT 50

10

NGNCGTTGTN GCTGCCAAGC GACAT 75

## (2) INFORMATION FOR SEQ ID :56:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :56:

25 AATNNNNNCC TATTTTGTA TTTTTTGAA AAAAGTTCAA TGTTCA GTTT 50

TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA 100

AAAAGATGCC TTTTACCATG AATTCTTGAG TTACATCAA TAATATTGTA 150

30

TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A 181

## (2) INFORMATION FOR SEQ ID :57:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

49

## (xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA 50  
5 GATGACGNNNA TCCAATTTC AACCACCACA GGGCACTGGC ACACAGAGGG 100  
GATTATTACA GAACCACTGA GATGACATTT 130

## (2) INFORMATION FOR SEQ ID :58:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20

GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA 50  
CATTGACAAG TACAAAAATT AAAAAATAT GCAGAAATAT TGAATAACTA 100  
25 GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT 150  
CCATGAA 157

## (2) INFORMATION FOR SEQ ID :59:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40

GAGGTGAAGT TGTCTTTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT 100  
 GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATT 150  
 5 TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200  
 AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250  
 CA 252

10

(2) INFORMATION FOR SEQ ID :60:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 198 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50  
 25 GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100  
 AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTCAACTT 150  
 TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:



51

GAGGTGGCAT TATGTGAGAC AGCATTGGT TAGGGAGTGC CAAGCATTCT 50  
ACAGCATTG ATGGTGGAAA TAGTCATGCT TTTATTTCT GCTCTCTAGG 100  
5 AATGTAAGGT GCACAGCAGG TCAGGTACT GCTGTGTGAG ACAAAGGTC 150  
CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA 200  
GAGTGCTTCT CATAACCTT CAGGAACCC 229

10

(2) INFORMATION FOR SEQ ID :62:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :62:

CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAA GGGACTGAAG 50  
25 AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA 100  
ACCGCTTAAT GAATTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGGC 150  
AAGAGCTTTT GGAAGTTTT TAGAACAGAA T 181

30

(2) INFORMATION FOR SEQ ID :63:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :63:

52

GTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA 50  
ATTGGCAGA AACAGAAAA GGACATGGGA TAACTTTAG ATTTAAAGAG 100  
5 GCAGGCTTGG AACACAACT GGTATTCTGC TGACACACTG CTGCATATCA 150  
TAAGGCTACT CCACAAGACC ATTAGAAGTC 180

## (2) INFORMATION FOR SEQ ID :64:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :64:

20

ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC 50  
AGGGAAGTGT GATTATTTAA AAATANGCNA GAACTTATTT CANCTGTGCT 100  
25 TTAGAAANAA NTGTATACGG 120

## (2) INFORMATION FOR SEQ ID :65:

## (i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :65:

CACATCGCTA TAATCCTTTC TGAGGACTTA AAACCTTATN ECACTTACCT 50  
40 TTATGACTTT TAACAAGCCT 70

53

## (2) INFORMATION FOR SEQ ID :66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :66:

	TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT	50
15	ATTTTCCTAA TCATGAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG	100
	GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC	150
	CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN	200
20	TCCACACACC CACACGATTT AGGAACTTGG ACATGTTTCCT	240

## (2) INFORMATION FOR SEQ ID :67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :67:

35	GGAAGCACTA CATTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT	50
	TACGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT	100
	TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT	150
40	AACCTATTTC TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG	200

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250

TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAGT GAAAGACTAA CCAAGATTTG 50

ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100

20 TCAACAAATN NNNACAACCTG AGAACCTGGG AATTCCCGCA CGGAAGACAA 150

GAGATAACCT CTCCAATTGA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAA CAAAGACAG GAGCAGAGAG GCCTGAGAGC 50

AGGAGGCGAA TTCGATCTCT CCTCACAAC AGCCCAGGAA AATATACACC 100

40 CCGGGGGAAG CC 112

55

## (2) INFORMATION FOR SEQ ID :70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTTAATCC TTGGGTTGTT TTACCACTTC TTTCGTAAAT	50
TTATCAAGAT TTCTTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG	100
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT	150
ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG	200
CAGATTTATT CCTTTAACTG ACATTTCAT GA	232

20

## (2) INFORMATION FOR SEQ ID :71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :71:

CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT	50
TTCACTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG	100
GAACCTTTGA GGAGATCGAC TGAAAGACTA GCGNCCNGT CAGATAAGAT	150
TTAGGGCTGA	160

40

56

## (2) INFORMATION FOR SEQ ID :72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT GGTTCGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC 50  
AATACGTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT 100  
CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGAAGT TTCGATTCTT 150  
TTTTCCTCCC GTCGCAAATT CTATGTTTGG AT 182

20

## (2) INFORMATION FOR SEQ ID :73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG 50  
ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA 100  
CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG 150  
ANAGGCTGCA CAATGAAA 168

40

## (2) INFORMATION FOR SEQ ID :74:

57

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC 50

AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCAGGGGTT 100

15

GTATACCACA CCCCAGGGCCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA 150

ACTAGTTCTT TNNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC 200

NCTNTCCCTN NAATAAATTN C 221

20

## (2) INFORMATION FOR SEQ ID :75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGTCAATCCGA GATCATTAAT AATGCTGAC CCTAACAATA 50

35

GGCACAAAAA TAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT 100

TAGAAAAAAA CAGGGCCTTG AGTTCTG 127

40

## (2) INFORMATION FOR SEQ ID :76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :76:

AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAACA TTTCAAACC 50  
10 CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACATGACC 100  
ACAAAATTAA TACTACCAA TCATTACTGA GACTCTTGCA TTACAATATT 150  
15 TGGAGAGTAG GTGAAGAAAA TNTAGACCGA 180

(2) INFORMATION FOR SEQ ID :77:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :77:

GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC 50  
30 GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAACTG 100  
TCACTTTAGC CNCNAACTAC AAGACCGTT AGACTAGAGA GC 142

35

(2) INFORMATION FOR SEQ ID :78:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID :78:

5 GGGCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC 50  
ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT 100  
CTGNCCCCC CNNGNCCCC CCG 124

## (2) INFORMATION FOR SEQ ID :79:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :79:

20 AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTTC A 50  
TATAGTCTAA AAGCTAGAAG AACAGAGTG TATTCGTGG GTGGATGTAT 100  
25 NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT 150  
TTAGNAAAN GCCNTTTTAA G 171

## (2) INFORMATION FOR SEQ ID :80:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 98 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :80:

40 CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA 50

60

CGACAGTGCC GTGNGGGCAC CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR SEQ ID :81:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15 CCTCAACAAG TGCAGACCT GGGCGTCAA CCTGCCTACA ACCACAGCCG 50

CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT 100

CAACATCA 108

20

(2) INFORMATION FOR SEQ ID :82:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC 50

35 CCTAAATTG TAAAGCTTAA TACAGTTNT GGAAATCATT TAACACCCGA 100

GAATGTCCCA TCACAGTCTT CCGTCAAAAT TTAGCCTCAC AACACAACA 150

ACGCCTACGA AATTCTAAAT TCAGAAGGAA 180

40

(2) INFORMATION FOR SEQ ID :83:

61

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT 50

CGATGCAGCT GCCATGCCGG CCAGAATCAG CGAAGGCATA CCCTTACGTC 100

15

GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC 150

CTTCTTAATA AACACCTCCT CGCCAATGCG GACGACCACA ATCACCGTA 199

## (2) INFORMATION FOR SEQ ID :84:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA 50

CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA 100

35

GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG 150

CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATT 200

NACNGAATAC AACC 214

40

## (2) INFORMATION FOR SEQ ID :85:

62

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10

CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC

50

AGTACCTGGG CATGTCCTGT GATGGCCCCCT

80

15

## (2) INFORMATION FOR SEQ ID :86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :86:

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC

50

CCTGAAATAC GCGCTTTTCA CTGCGTGCT CAGAGCTGCC GTCTGAAGGT

100

30

CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT

150

GATTAGTCAG TTTTCATTTA TAAAAAGCA TGACAGTTTA TTA CTCTGTT

200

35

TCTTTTAATG

210

## (2) INFORMATION FOR SEQ ID :87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

63

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT 50  
ATTTAAAAAT ACTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA 100  
10 CA 102

(2) INFORMATION FOR SEQ ID :88: ---

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25 GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT 50  
ACGGGCAGTG AGAACATTAT CTGTATAACA GGAAGTGTGA TTATTTAAAA 100  
ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA 150  
30 TAAGTTGAAA AGAACTCAAA ATAAC TAATA CAAATAAGAA CCTACGTATT 200  
AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAATAAAA 250  
35 TGACACAAAT TCAAAACACG ATCAT 275

(2) INFORMATION FOR SEQ ID :89:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA	50
TTAATAGTAA TTATGGTTTG GNGTAAAT CGAGTTTCAG AATAAAATNA	100
10 AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAGCT TTTGTTTTGT	150
TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTTCC	200
15 TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT	250
GCTGTGTACT CCA	263

(2) INFORMATION FOR SEQ ID :90:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :90:

30

GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC	50
CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCC CGAGGGACCC	100
35 CTTTGAGA	108

(2) INFORMATION FOR SEQ ID :91:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

65

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :91:

GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT	50
ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA	100
10 TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTTCAG AGCACCACAG	150
GGCACTGTGT ACACATGAGG GGTACCTTA CAGAGCCACT GAGAATATAT	200
15 TAATAA	206

(2) INFORMATION FOR SEQ ID :92:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 210 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

CCTTGGTGGA GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA	50
30 TGGCTTTGGC TGATAGATT GAAGAGACCT CAATTACGTT TTTCAGGAAT	100
GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG	150
35 GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT	200
AATAAANNNG	210

(2) INFORMATION FOR SEQ ID :93:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

66

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :93:

AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAACT AACCTAAAAG 50  
10 GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA 100  
AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGTCCTGT 150  
15 GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG 189

## (2) INFORMATION FOR SEQ ID :94:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :94:

GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTGTAA ACTAACCAAG 50  
30 CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC 100  
TCAACGCATG ACAAAAAACT CAGGACTGCA TTGCACTAA TCGATAACGN 150  
35 GTCATTTAAT 160

## (2) INFORMATION FOR SEQ ID :95:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



67

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT 50

AAAAGGCAAC AATTTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT 100

10

AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTTT 150

TAAGGAAACT ACAGAAGGGA T 171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT 50

TTCCCCAACC TTTTATTTCG CGAAGAACT CCAGTTGTTA ACTTTTGGAG 100

30

AGTTTTTTTT GGCAAAGAA CTNCATTAN C 131

(2) INFORMATION FOR SEQ ID :97:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

68

## (xi) SEQUENCE DESCRIPTION: SEQ ID :97:

5           GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA           50  
          GTAAAGTTAA GGCACGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA           100  
          CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN           150  
          TTACTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC           200  
10           ATAATGTATT GATGATCTGC TGTAACCTTG AGAAGCTTCC TGAAGCTCNT           250  
          TTTGAATAAA TTTATNGAAC TTATGAAGA           279

## 15           (2) INFORMATION FOR SEQ ID :98:

## (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 266 base pairs  
          (B) TYPE: nucleic acid  
20           (C) STRANDEDNESS: double  
          (D) TOPOLOGY: linear

## 25           (xi) SEQUENCE DESCRIPTION: SEQ ID :98:

          GTGAGTCTTT CTTCAACTAG GGAATGTTT CCAGGGCAGC CCAGGCCTCA           50  
          CTCACGCAGG CCTCCGCGAC AACTGTTCAG CACTGACTGA GGATGAAGTG           100  
30           AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA           150  
          CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT           200  
35           GACGAGACCA GGACCCTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA           250  
          AACTCCAGGG CCTCCA           266

## 40           (2) INFORMATION FOR SEQ ID :99:

## (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 206 base pairs

69

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA 50  
10 ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTTGGT AAAAAATATA 100  
TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA 150  
15 GTGCTTACCC CTGGAAGGG GGTATACGAT GTTGATTAC TCTTTGGGTA 200  
CGTATT 206

(2) INFORMATION FOR SEQ ID :100:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

30

CGCAACTNTC NCTAAACATC CAGTTTCTA ATNTAATAAA AAATGGCAGT 50  
AATTATCCTC ACCTCTCAGG GAA 73

35

(2) INFORMATION FOR SEQ ID :101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

70

## (xi) SEQUENCE DESCRIPTION: SEQ ID :101:

5 GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50  
ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT 100  
ACTGCCCC 108

## 10 (2) INFORMATION FOR SEQ ID :102:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTAA TTTTCCAGCT TTGATCTTAN 50  
NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTCTCA AACGATNTAT 100  
25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150  
TCAATATAAC ANAAAAAGGN ATTTTGCAAA AAGTACAAGT TTTATGTCTN 200  
30 CTGTTAAGTG 210

## (2) INFORMATION FOR SEQ ID :103:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT 50

GTCACCAAAA TTTCTTTCCA AAAAAA 76

## 5. (2) INFORMATION FOR SEQ ID :104:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAA TCTTTCATAG AAAGATATTA TCAAAGCTGA 50

AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA 100

20 CCGATTGAAT GGTTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC 150

AAGTCGCAAG GAACATC 167

## 25 (2) INFORMATION FOR SEQ ID :105:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC 50

CTCACGGGAC CACCATCATA CAGCAATTTG TCATGATCAA AAGAAACATC 100

40 ATTAGTCGTG CCATAACTGT AT 122

72

## (2) INFORMATION FOR SEQ ID :106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCCTTCA CTCCAGATT CCAATGCCAA GATACATTGA TACTGAACAT 50  
GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCACCC TCACAGACTC 100  
ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA 150  
GATGATGTTA TTTACAAGTG TTTATGGATC ACTGAAGAA ACTTGCTGTG 200  
TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA 250  
AATAA 255

25

## (2) INFORMATION FOR SEQ ID :107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGAATA TTTACAAAGA AAAGTGT TTT CTCAAAACAC 50  
TGTTTCATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA 100  
AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT 150

73

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT 200

ATACCAAGAN ACANTTATGT GGTAAAT 227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTTNNNN NGCCATACCA TGGTACAATA 50

ATCATNAAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA 100

20 CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAAAA ATAGNAAAAA 150

AAAAAAATAA CA 162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA 50

AAATAAAAAA CGAAACCCGA GAACCAAAT GAACGAAAT CTTTCGCTTC 100

40 ATTCATCGTC CCCACAATNC CAGGCTACC CCCCATCTG ATCATTATT 150

GTTT

154

## (2) INFORMATION FOR SEQ ID :110:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15 ATGTGCCAAG TAAAAAATCA ATTNGTNGCC TTTTCCATT NCGCGGACAC 50  
CCATAGGCAC CAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG 100  
AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT 150  
20 GCACTCCTTG TTAATAACAA TACACTATAT CA 182

## (2) INFORMATION FOR SEQ ID :111:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35 GAAGGTGAGA ATAGGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA 50  
CNTCAAAACC AATGGTAGAA CATCACATTT CAACTGCAA ACCA 94

## (2) INFORMATION FOR SEQ ID :112:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 92 base pairs



75

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10

TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT 50

GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT 92

(2) INFORMATION FOR SEQ ID :113:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25

GATTGTTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG 50

TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG 100

30

ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAACTCCAA GAATCTAGAG 150

GG 152

(2) INFORMATION FOR SEQ ID :114:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

76

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTTCAGTG 50  
5 TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG 100  
GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA 150  
TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA 182

10

(2) INFORMATION FOR SEQ ID :115:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :115:

GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC 50  
25 TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC 100  
AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC 150  
TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT 182

30

(2) INFORMATION FOR SEQ ID :116:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 227 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :116:

77

GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTG ATAAANTAAC 50  
ATACAAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA 100  
5 TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT 150  
ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA 200  
TGGAAATAAG CTAGCTACGC TCAATGC 227

10

(2) INFORMATION FOR SEQ ID :117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :117:

CGAGAGATTG GTAATGAGGA AGCAATTGG AGGGGNGGAA GCTACAANGA 50  
25 NNNNGGGAAT TACAACAATC AGTCTTCAAA TTTTGGACCC ATGAAGGGAG 100  
GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC 150  
TTGCAAACC ACGAAACCAG GT 172

30

(2) INFORMATION FOR SEQ ID :118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

78

AATGATGGAA GCAATTTTGG AGGTGGTGA AGCTACAATG ATTTTGAAT 50  
TACAACAATA GTCTTCAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG 100  
5 GCAGAAGCTC TGCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG 150  
AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG 200  
GCAGAAGATT 210

10

(2) INFORMATION FOR SEQ ID :119:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT 50  
25 TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC 95

(2) INFORMATION FOR SEQ ID :120:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

GGAGTATTN AANNITTCAA ACTTTATTAC TTAATGAAAC AGTTTCTATA 50  
40 TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTTTTTG 100

79

TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTTT ATTAAGTCT 150

TCCAGAAACC GTAACAGG 168

5 (2) INFORMATION FOR SEQ ID :121:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTTA TCTTTCAAC TCCNACTNA GTGAAACAGT TTCTATACCA 50

CTGCTTCCAA TTACTANCTN TTTTNCNGT TAAATTTTCN NCTGTTTTTC 100

20 AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA 150

ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA 200

25 ATACATACTT CGGTGACNTT ATGCATCATG A 231

(2) INFORMATION FOR SEQ ID :122:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT 50

40 AGCTGTTTAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG 100

80

ACACCATTGT ACGGTGTACA ATGTCATGGG ATCAGGTGTT CAAACTGATT 150

GGAATCTTTC TGAAAAGGAT ATGA 174

5 (2) INFORMATION FOR SEQ ID :123:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAAATG TTCTGTTATC 50

20 AACTGNNTTT ATAAAAAATC GATTGTGGGT AGAAGCAGAG AAAAGGCACT 100

TAGTAAAGAT ACTACATGAN GAAAAANNTC TGCCCTTTGA ATTCTTANGA 150

AACATNNTNG NNGAATCAAT 170

25 (2) INFORMATION FOR SEQ ID :124:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNTTTATAAA 50

40 AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACTTAGTA AAGATACTAC 100

ATGANGAAAA ANNTCTGCCC TTTGAATTCT TANGAAACAT NNTNGNNGAA 150

81

TCAATNT

157

(2) INFORMATION FOR SEQ ID :125:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15 CAACTTGAAA TACATTATGA TGTCTGATAT GATTAAATAT CATTGAGNAT 50  
CTTGCAAACA AAAAAAGCAA AAAATTAAAT CTCCATATCA ATCTTAAATT 100  
CTTGGCATAT TTACTTCTGG TAAATATTAC TTCTGGTCCT TATTCTATAT 150  
20 GTGTTATTGA AATTGTGTT 169

(2) INFORMATION FOR SEQ ID :126:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35 GTTTNGTTNN NNNNTGTTCC ACCTTTTGTT GAATTTTAGT TGTTAGGCTG 50  
AACCTCCGAG CAGTTTNAGG ACTGCCTGA GTTTTCTTC 90

(2) INFORMATION FOR SEQ ID :127:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG 50  
10 AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTGAG CAACTTGACA 100  
TTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT 150  
15 AGGAAAACCA 160

(2) INFORMATION FOR SEQ ID :128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :128:

CCCCCAACT TACATCCTCA TTATTGGCGC CTACAACTC AACTACGAAC 50  
30 ACACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTA CTGGCT 100  
ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC 150

(2) INFORMATION FOR SEQ ID :129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40



## (xi) SEQUENCE DESCRIPTION: SEQ ID :129:

5 AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNG NTTCCGAAG 50  
CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA 100  
GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA 150  
10 TGAAAAACCC AAAACAGTTA CGANGCTAAT CC 182

## (2) INFORMATION FOR SEQ ID :130:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :130:

GGACCATCTT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50  
25 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC 100  
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150  
30 TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA 200  
TGCTTACTTC AAGAAGAAG 219

## (2) INFORMATION FOR SEQ ID :131:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

84

## (xi) SEQUENCE DESCRIPTION: SEQ ID :131:

5 AATAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAA 50  
GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT 100  
CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT 150  
AGAACATCGT TAACGGAATC ACAGATATAT C 181

10

## (2) INFORMATION FOR SEQ ID :132:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT 50  
25 GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG 100  
TAGAAGATGN AAACAACTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG 150  
CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC 188

30

## (2) INFORMATION FOR SEQ ID :133:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :133:

85

GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGA CTGACTTGT TCTGAGCAAC 50  
TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT 100  
5 CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTTCAC AGAAGCTCTG 150  
TGA CTGACTTGGTT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC 190

(2) INFORMATION FOR SEQ ID :134:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20

ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC 50  
AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC 100  
25 CAGGGTCCAT TTAAC TAAGA GGTGGTGATC TCCACGCCAG CCCCAAAGAT 150  
GTCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA 200  
TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG 235

30

(2) INFORMATION FOR SEQ ID :135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

86

GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT 50

ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC 100

5 AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG 147

(2) INFORMATION FOR SEQ ID :136:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :136:

GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA 50

20 CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG 100

NTCCCACTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA 150

25 CTNAGAATGC GGAGGAGATC T 171

(2) INFORMATION FOR SEQ ID :137:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :137:

ACATATATGT GGTAGGATAG AGAGATGGNN NNNGTGTATG ACATAGGTGT 50

40 TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTC 100

87

TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTGAGTCT ---150

GTAAGTAGG 159

## 5 (2) INFORMATION FOR SEQ ID :138:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAATA AAACACGAC 50

NCACTCACAA TCGCTCATAA TCTCTTNAAG ACTTCAAAT NTCTCTNTGA 100

20 NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCCNTGTNC 150

TNCGGGAGAA CTCTCTGTGC TGTACCACT 179

## 25 (2) INFORMATION FOR SEQ ID :139:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC 50

TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG 100

40 ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA 150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

## (2) INFORMATION FOR SEQ ID :140:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAATCAT GGATTATAAA ACATTTGTGA 50

CTTATACTGT CTNTGTCAGT TA 72

## (2) INFORMATION FOR SEQ ID :141:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30

GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTA AGTATTNGTT 50

TTAGTACGNA AA 62

35

## (2) INFORMATION FOR SEQ ID :142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5 ACCAGTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT 50  
GGTCAGCTTC TCTTCTTTA TCTTCTTTC TCCTTTTTA AGAAAACGAG 100  
TTAAGTTTAA CAGTTTTCGA TTACAGG 127

## 10 (2) INFORMATION FOR SEQ ID :143:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :143:

AATATAAAAG ACAGCAGTTT CACATTTTAC ATATTGAAA AACATTTCAA 50  
AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT 100  
25 GACCACAAAA TTAATACTAC CAAATCATTA CTGAGACTTT TTGCATTACA 150  
ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATT 198

## 30 (2) INFORMATION FOR SEQ ID :144:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :144:

GTTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA 50

90

AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG 100  
TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG 150  
5 AACTGCTTT GTATCTGCTT TGNA 174

## (2) INFORMATION FOR SEQ ID :145:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :145:

GAGAAATAGT ACTTTAAAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT 50  
20 AAGATTCATA AAATGTACCT TTTTGTATTG TTTTGTTCIN GAGTTTTCGA 100  
TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA 150  
25 TTTTGG 156

## (2) INFORMATION FOR SEQ ID :146:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :146:

AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50  
40 GTTGGAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100



91

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT 150

T 151

5 (2) INFORMATION FOR SEQ ID :147:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAATC 50

CAGGTAANNT GGTTCGATCT GATCGATTG GCTGCATACT TTCGGTACGT 100

20 ATACATTCT AAACCTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG 150

TAAAATTTTA AAAGTTAAAG TACTAGC 177

25 (2) INFORMATION FOR SEQ ID :148:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT 50

TGGAATGG CTGTTTTGTT AAAATATATC TTTAGTGTG CTTTAAAGTA 100

40 GATAGTATAC TTTACATTTA TAAAAAAAT CAAATTTTGT TCTTTAAT 148

## (2) INFORMATION FOR SEQ ID :149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50  
GTTGGAAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100  
TAGATAGTAT ACTTTACATT TATAAAAAA ATCAAATTTT GTTCTTTATT 150  
TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA 200  
ATCC 204

20

## (2) INFORMATION FOR SEQ ID :150:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :150:

AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATCAATAGGA 50  
TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT 93

40

## (2) INFORMATION FOR SEQ ID :151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :151:

AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT 50  
10 ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC 100  
CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAC CAGGAAGGTG 150  
15 T 151

## (2) INFORMATION FOR SEQ ID :152:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :152:

TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCT 50  
30 CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA 100  
TGTAGCCTC 109

## 35 (2) INFORMATION FOR SEQ ID :153:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :153:

5 AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50  
TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100  
AGGAAAAGGG GAAAAAACC CATAATGGGC CTAAAA 136

## 10 (2) INFORMATION FOR SEQ ID :154:

## (i) SEQUENCE CHARACTERISTICS:

15 ---(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50  
CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100  
25 TCAAGATGAG TATACGCATC TATCATTGCA ATTGTGTCAT TAATTGTAG 150  
GGCCTCATTG 160

## 30 (2) INFORMATION FOR SEQ ID :155:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

ACCACTNNNN NNNGGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA 50

95

ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTNTCT TTTCTCCTTT 100  
TTTAAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT 150  
5 GACTTCATGC TTAGTGTAAG GTGGAAGTTG AGATATTTTA A 191

## (2) INFORMATION FOR SEQ ID :156:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :156:

CAACTGAACG CTTTGGTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN 50  
20 TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT 100  
GCCCCAACA AACGTCGCCG ATACTAATAA GTTGCACTG 139

## 25 (2) INFORMATION FOR SEQ ID :157:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :157:

GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA 50  
CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNGC AGGCAATCTT 100  
40 TCTTTTGTTC ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA 150

96

AGCACCCGCA AATTACCTT TG

172

(2) INFORMATION FOR SEQ ID :158:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15 GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT 50

CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG 93

(2) INFORMATION FOR SEQ ID :159:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30 GNATTTTTTT ATTGATATAT CATAGTTGTA CAAACATTG GGAGTNCANG 50

TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC 100

35 CA 102

(2) INFORMATION FOR SEQ ID :160:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

97

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA 50  
TAGAAGCAAT AANNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT 100  
10 ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT 150  
ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA 200  
15 GCGGA 205

(2) INFORMATION FOR SEQ ID :161:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA 50  
30 AGTTGTTTTT CATATAAAAA ANNNNNNTGA TTTTAAAAA ACTAANNAAC 100  
TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAAGTGG GNCACCAAAA 150

35 (2) INFORMATION FOR SEQ ID :162:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :162:

5 TATTCAAAAG AAAACATGG GTAAAAATGA TAGTGTTAAA TCTTGGCTCT 50  
GTGTACATAG ATAGATACCT GTTACAG 77

## (2) INFORMATION FOR SEQ ID :163:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :163:

20 GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT 50  
TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT 100  
AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTTCT 150  
25 CAAACTGACA TGCTACAGAA ATGTCTTCCA AA 182

## (2) INFORMATION FOR SEQ ID :164:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :164:

40 GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA 50  
TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC 100



99

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT 150

CAGATTCACA GACATTGCA AACAGAAGA TG 182

5 (2) INFORMATION FOR SEQ ID :165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT 50

GAGACATATA TACCACCCAA GTTTTAACAC CATATCCCAT CGGCTGTTAG 100

20 TGTATATAAA AAGAAATAA 119

(2) INFORMATION FOR SEQ ID :166:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTCC AACACATAG 50

GATCCCATCT CAGGAGCAGG ACCAGTGTTT AGCTAGATTA AACTTCGCTG 100

GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA 150

40 AGATGTTATG GCAGAAGTGA CTGTTTTGTC TCAACAAGCA TTG 193

100

## (2) INFORMATION FOR SEQ ID :167:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGAGAG 50  
GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT 100  
GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT 150  
TAAATGGACA GTTTATAAAG TGTCTGGP GCCGA 185

20

## (2) INFORMATION FOR SEQ ID :168:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG 50  
TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG 100  
ATTCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA 150  
ATTTTAAAA ATA 163

40

## (2) INFORMATION FOR SEQ ID :169:

101

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10

AGACAAATTC NNNNTNNNN NTGCCTGATA ATTCAGATG CCACCGTATA 50

GCAAAGGGTG AACATGTTTT CAACCCTTA ACTTTTACG GTGTTTGAAG 100

15

ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG 150

CAGATTTACA ATTGGGTTT TTGTCTGGAG TTGCTCGGT TTGAAGCCCC 200

CT 202

20

## (2) INFORMATION FOR SEQ ID :170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :170:

TCAGGGAACC AAAAACTGG CTGCTTGGC ACCCAGGGAC AGTAGCTGTT 50

35

TGGCTCTCCA CCCAATTAA AAAACAAATC CCTGCCCTTT CCCCCACCCC 100

ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT 150

GGTGCCCAAG GCTGTAAA 168

40

## (2) INFORMATION FOR SEQ ID :171:

102

## (i) SEQUENCE CHARACTERISTICS: —

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10

AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA 50

GCAATTTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCRAAC 100

15

TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT 144

## (2) INFORMATION FOR SEQ ID :172:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :172:

ACCCACAGNN NNNACCTAGA GGCCAGCGC CCAGAGAGGC ACGTAGAAAT 50

30

GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A 91

## (2) INFORMATION FOR SEQ ID :173:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

103

## (xi) SEQUENCE DESCRIPTION: SEQ ID :173:

5 GATTTTTTAA TGGGTNGCCT CTTTGTAGCTT GGAATATTAC GTTTACTTTA 50  
ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT 100  
GAATCCCTTT GACATCTATT ACAGGTATA GGACCTTTTT GGTGTGATTA 150  
CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTTGGCA GAAGTTAAAA 200  
10 TGGA 204

## (2) INFORMATION FOR SEQ ID :174:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :174:

25 GTAAATTCA CTACATCTTT TNNTNGACT TTCATGCATT TCTCATACAT 50  
TNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTAA 100  
ACGAAAGGCG GTTCAATTCA TCAACTGAA ATGACTATTT ATTTTNNAGG 150  
30 ATTTTTTAGG GGAAGAGTAC CCATTCGTT TATAAAAACA GATGACAAAT 200  
TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G 241

## 35 (2) INFORMATION FOR SEQ ID :175:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

104

## (xi) SEQUENCE DESCRIPTION: SEQ ID :175:

5 GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT 50  
TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT 100  
AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC 150  
10 TTACAGGTTT CTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT 200  
TTGGCCCTTT T 211

## (2) INFORMATION FOR SEQ ID :176:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25

AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG 50  
NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN 100  
30 TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA 150  
AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTCTT GACCTATGAT 200  
AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA 250  
35 AT 252

## (2) INFORMATION FOR SEQ ID :177:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid

105

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA 50

10 GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG 100

TTGCAGCCAA TCTTCTCAA GCAAACCGAC TTCCTAACAA CTNTCTACAT 150

CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA 200

15

TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC 250

ATCTGAAGAT ACCAGCTTCA AATACTAAT 279

20

(2) INFORMATION FOR SEQ ID :178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :178:

TATGCCCTGA AATGAAACCT CTAAGTTTGA CAAAATACCC AAAAAACAG 50

ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTG GTGGGTGGTC 100

35

GTTCTCAATT TATAAANAA TAAATGACTT TAAAGGAGAA ATAAATTAT 150

GTCAGGA 157

40

(2) INFORMATION FOR SEQ ID :179:

(i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10 GATAATGCAA CTTTGGACAG GAAAGCGCGA TTTTACTAT

39

(2) INFORMATION FOR SEQ ID :180:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

GCAAACTCAA ACTACGGACG CACTCACAAAT CGCTCATAAT CCTCTCTAAG

50

25

GACTTAACT CTACTACACT AATACTTTTT GATGACTTCT AACAGCCTC

100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG

150

30

TACCACA

157

(2) INFORMATION FOR SEQ ID :181:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:



107

CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA 50  
CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC 100  
5 ATTCTGGTAA AACTGGAAG ATGACCCTAA ATTTGAAGT TGATGATGTG 150  
CCATGTGATA TGGTCTGAC AAACCCATGT GCGTTGAGAG CTTT 195

## (2) INFORMATION FOR SEQ ID :182:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20

CATGGTCTTA ACCAGTGTCA GATGGAATCA GTGGATAAAT CCCCAGGTTT 50  
GTTTGTCCCTT CAAATGGGAC AATTGAGGA ATGCTTTAGG CAGAGGACTC 100  
25 AGATGACAGA GCGCCAACCA CCCACAATAG AAACCTGCTC ATCACA 146

## (2) INFORMATION FOR SEQ ID :183:

## (i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :183:

TAGAGGAATA GGGNNNGNGA CGCCCNAGT TGTAGGGACG GACGGAGGAC 50

40

## (2) INFORMATION FOR SEQ ID :184:

108

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10

ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC 50

AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG 100

15

CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT 150

GTCCCCTATG ACGACGAGAA TGTGATTATC TGAAGCAAC TTGATCTTGA 200

TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT 248

20

## (2) INFORMATION FOR SEQ ID :185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :185:

AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT 50

35

ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTGT 100

AACGTGGCTT TCT 113

## (2) INFORMATION FOR SEQ ID :186:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs

109

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTCC CAGGATCCCG 50  
10 ATGTCGTCAT ACACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC 100  
ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC 148

15

(2) INFORMATION FOR SEQ ID :187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :187:

TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG 50  
TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA 100  
30 GCCAACTACA CTCCCACTGC TAAAAAGATG AAAGGACCAA TCAAAGATTT 150  
AATTAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC 200  
35 TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC 248

(2) INFORMATION FOR SEQ ID :188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTTC 50

GTTTAATACA TAAGTGTCCA ATAATAATGT CAACCCTCCC TCGCCACAGC 100

10 CAATAATTTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT 146

(2) INFORMATION FOR SEQ ID :189:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25 ATTTACCACA AGGGACGATT TCCACACCAA CCCC AAAAAT GTCCCCTATG 50

ACGACGAAAT GTGTATTTGA AACAGCTCTG A 81

(2) INFORMATION FOR SEQ ID :190:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

40 AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA 50

111

GAGCAAGAAT TGAAGATGCA CAAACTTCGT TCTGAATTG TGAGCTTCCT 100

GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA 50

20 ATGGGGCATA CGAGTAATAT GTACATATCA AACAATCAAT TGCCTCCTGA 100

AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA 150

CA 152

25 (2) INFORMATION FOR SEQ ID :192:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTTGAT TGCGTAGTAA GGTAAGACG ATTTTATAGA 50

ATNAAGGTGA TTCCT 65

40

(2) INFORMATION FOR SEQ ID :193:

112

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10

AGGACCCAAA CTACCTTATT GCATTGAAG TTTTACTTAT NCTATTATAA 50

TCTAAGAGCC CACCCAACAA GGCCTACAC ATAGATGCTC ACACTCTATA 100

15

GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG 150

CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC 200

TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA 249

20

## (2) INFORMATION FOR SEQ ID :194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :194:

GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG 50

35

TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC 100

GCTGCATATG TGA CTGTCAT GAGATCCTAC TAGATGATCC TGACTAGAAT 150

GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT 194

40

## (2) INFORMATION FOR SEQ ID :195:

113

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10

GTGATTTTAG TTAAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA 50

TTTAAGTCAC ACACATAGTT AACAAACNCNC GTNGCGTGCA ATAAATACCA 100

15

CATCCTTTNA TATGNNCNGN A 121

## (2) INFORMATION FOR SEQ ID :196:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :196:

GGGCTTCNNN NNNNNNCATG TCACTTAGA ACCGTTACTA ACCGAAACAC 50

30

CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT 100

AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA 150

35

TTGTGACCAC AAGTCTTGTT TCTTG 175

## (2) INFORMATION FOR SEQ ID :197:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :197:

ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG	50
AATCAGAGGT ATCAATGAAA TGAGCCCCAA GGTTCGAAAG CTCGCAACTT	100
CTTCACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT	150
ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA	200
AATGACTAAT CTACAAGCNT GTTATGCAA ATAAATAAGA AACGACTTGC	250
TTACAGATGC NTTTTAATTG TGG	273

20 (2) INFORMATION FOR SEQ ID :198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT	50
GNTATA	56

35 (2) INFORMATION FOR SEQ ID :199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear



115

## (xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5 GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG 50  
GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC 100  
CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA 132

## 10 (2) INFORMATION FOR SEQ ID :200:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :200:

AAACTTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC 50  
GACATTTCAA TCGNACACAA ANTAAAAAA TAAACAAAT TTAAAAAAC 100  
25 CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTCCAAC TTAAATTCA 150  
GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG 200  
30 CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN 250  
TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT 284

## (2) INFORMATION FOR SEQ ID :201:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

116

## (xi) SEQUENCE DESCRIPTION: SEQ ID :201:

CCTGACACCA ATTCGCCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA 50  
5 AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTNT 100  
CTTGNT 106

## (2) INFORMATION FOR SEQ ID :202:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20

CTTTGAAAA CAAACATTTN TTATTACTGA AATAGCAAAA ATCATTCTAC 50  
ACTCCTCCTA AGCATGTTCA ATTAGCATAC ATTCCAACAA TGCATGAAAA 100  
25 AATTNCTAGC CAGAGGCATT TAAGTGATT CTTCCTAAGT GTTGCTAAT 150  
TCAATGCCAA GAACTATGAT GTTATCNTT CTGATGGACA AATCAAGAAA 200  
CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT 250  
30 CATTACTCTA ACTGTTAATC 270

## (2) INFORMATION FOR SEQ ID :203:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

117

## (xi) SEQUENCE DESCRIPTION: SEQ ID :203:

AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA 50  
5 AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA 100  
ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAAACTG ATTTTACTT 150  
TACAAAANNG NAATTTGCAA TTA 173

10

## (2) INFORMATION FOR SEQ ID :204:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :204:

CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN 50  
25 ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT 100  
CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT 150  
CATTACATT ANTT 164

30

## (2) INFORMATION FOR SEQ ID :205:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50

AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC 50

ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100

20 TGGGGTTAGN TGTTCNAA 118

(2) INFORMATION FOR SEQ ID :207:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAAGN ATCTTTTTTAA 50

TAAAAATACC TCTTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCG 100

AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150

40 GCTATGCATA ATACCCTCAC 170

119

## (2) INFORMATION FOR SEQ ID :208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA TGCTTGATA CAATGATATA ACAAAGAAAC CCTAAGACAA 50  
CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATTT 100  
TTTCTCGGGG AAGTAACCTT GCCTTTGAA 129

## (2) INFORMATION FOR SEQ ID :209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :209:

CTTGCGGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG 50  
GATCCTTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT 100  
CCAAATTTTG GCTCCAGAGT CATTCTGAA NNTCTACACT TANGGNCTTN 150  
AGCNTGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT 190

## (2) INFORMATION FOR SEQ ID :210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs

120

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

TCATTGAGTC ATCCTTTTTG CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG 50  
10 TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCCTACT 100  
GATGCAGAAC TGTTCATAT CTAGAAATG 129

15 (2) INFORMATION FOR SEQ ID :211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG 50  
CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG 100  
30 AAATGGAANC NNNGNGTTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT 150  
GG 152

35 (2) INFORMATION FOR SEQ ID :212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

121

## (xi) SEQUENCE DESCRIPTION: SEQ ID :212:

CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG 50  
5 TCGAAAGATG AAAACAACCTA AGTTCATAAC CCCCTGCCCCG CCATTGACCT 100  
CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTACATC 150  
10 NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT 186

## (2) INFORMATION FOR SEQ ID :213:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :213:

CTTAAATGCC TGTTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA 50  
25 CCTTTCTCTA AAATTCCTTT CCTTGCCTC CTCCTCTAAC TTTTCCTCCT 100  
TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTGG CTTCACTCTA 150  
30 TT 152

## (2) INFORMATION FOR SEQ ID :214:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

TCTTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG 50  
ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACTC CCACCGTATG 100  
5 TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC 150  
ATATTACATA TTTATAACAT TAATACTGG AAAAAGTGAA ATGCATGTCT 200  
GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT 250  
10 ATTATTCAAT AGTGGAATG ATGACTACAG CTATACCTCA 290

## (2) INFORMATION FOR SEQ ID :215:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25 GTTCTCTCCA GTACATCCAA GTTAAAATT ATTAGCGAAA TGGTCCATGT 50  
TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGAAGATCT 100  
GAGAGCATGC TGTGTTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC 150  
30 TGGGCCTCAC TTTACCCCAT TCGTAAAATG GGGATAATGT CACCTGCCTC 200  
TTACCTACCT CAGAGGGATT TCGAAGCAA ACTGTTAATC TTCGAAAACG 250  
35 ACCATTTACT TTTAGGATAT CAA 273

## (2) INFORMATION FOR SEQ ID :216:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT AGGGAGAAAC AATGTTCTTA CATATTATGG GTAGTGAGAA 50

CATTATCTGT ATAACAGGGA ACTGTGATTA TTAAAAATTA TGCAGAACTT 100

10

ATTCATCTG TGCTTTAG 118

(2) INFORMATION FOR SEQ ID :217:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25 GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAGAAGA AAACAAGTCT 50

ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTCACGAAA CCCTTTTAAA 100

TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAATAAA NGNNNTGATT 150

30

TACCACCAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA 197

(2) INFORMATION FOR SEQ ID :218:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218: —

CTCGCGAGCA CTCGTCCGAG AGGTCCCATC CNNNNNNNCC CAAGCCCCTC 50  
5 AAGGGCCTTT GCCAATCTNG TCATTTTATG CCAAGTCCTC TAAACGCAC 100  
TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC 150  
TATTTTAGGC TNCNAGGTCA AAATAAA 177

10

(2) INFORMATION FOR SEQ ID :219:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :219:

GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA 50  
25 GAAACCTANT AGTTCAACAA ATTAAAGAA AGAAAGAAAA AAAGCAAAAG 100  
TNGGTNTCAG GGCTGGAC 118

30

(2) INFORMATION FOR SEQ ID :220:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :220:

GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTTT 50

125

ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAAGTGA 100  
CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT 150  
5 TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN 200  
NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA 233

(2) INFORMATION FOR SEQ ID :221:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20

GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA 50  
ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA 100  
25 GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA 150  
CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAAACCTG 200  
TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT 235

30

(2) INFORMATION FOR SEQ ID :222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

-----  
GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG 50  
CCTTAGGAAT TGANTGAGGA CTAAATTTC CCCNGAGGGA GAGNAGTGGG 100  
5 G 101

## (2) INFORMATION FOR SEQ ID :223:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :223:

ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC 50  
20 ATGTCGTAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT 100  
TGACCAATT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT 150  
25 TTTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA 200  
ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC 250  
CATTCTTGAG ATACCAGCTT C 271  
30

## (2) INFORMATION FOR SEQ ID :224:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA 50

ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA 100

5 T 101

(2) INFORMATION FOR SEQ ID :225:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :225:

TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT 50

20

AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA 100

GACCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTTCA A 141

25

(2) INFORMATION FOR SEQ ID :226:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :226:

ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG 50

TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG 100

40

TTCTGTTATG TGCAAAGTAG ATTATTTTCA ATTACTTGG TATGGAAAGC 150

128

AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200

AAAANGCTGT TNNAAAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAACTTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNGGTGG 50

TGAGAAGTTG GTATTNATAG CACCTTATT ACATGATGGA CTTGAGGAGG 100

20 CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT 150

TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG 200

25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50

40 ANCATTTTCG CCAGAATGCT GTAATGNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTTT TTTTAAATG GTAAAACCCC 150

TTTTTACTGG NCNTTCCAGA ANCTTACAG 179

5 (2) INFORMATION FOR SEQ ID :229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCAAGT TATTGTAGCA GTGAAACAAT 50

GAGGGCATAC ACTATATNGA AAAAAAACC TCCTCCCTNA TTCTCAGCC 100

20 AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA 150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA 184

25 (2) INFORMATION FOR SEQ ID :230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTT 50

TTTTTAGGTT TAGAATTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTTA 100

40 GTGCAAACAT TGTTGAGTAT GTTGTCAAAC GTCTAAAAA 140

130

## (2) INFORMATION FOR SEQ ID :231: -

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT 50  
15 CCTAAGGCAG GAAGATGGTG GCNNNTNNNG ACGAAAAAGT CGCTGGNGNN 100  
NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG 150  
GGGGTAAAAG NAANATNNGA ANATGGAT 178

20

## (2) INFORMATION FOR SEQ ID :232:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AACNCNTAC 50  
35 CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT 100  
NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATTT TATANCTTCN 150  
NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG 200  
40 GCAACCANGG 210



131

## (2) INFORMATION FOR SEQ ID :233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :233:

ACTGTGCGAG TAGCTTNAAA ANNNNNNNNN NNACTCAGTT TNATTATAC 50  
AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC 100  
CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG 150  
ACTNTCTNAC NTTCAAACNA NTATTNCACG TAAAAACAT CACAGTGC GA 200  
AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG 247

## (2) INFORMATION FOR SEQ ID :234:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :234:

AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT 50  
GTGGACATTG GAATGTTTAC TGTTATTCTG TGTAAGAAAA CAACTNACAA 100  
AAAAGAAAAA TGGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC 150  
NGGGGGAAAN TGCCNGGGC 169

132

## (2) INFORMATION FOR SEQ ID :235:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANCACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA 50

15

G 51

## (2) INFORMATION FOR SEQ ID :236:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTAAG TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC 50

30

TCAAACCTTTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA 100

A 101

35

## (2) INFORMATION FOR SEQ ID :237:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

133

## (xi) SEQUENCE DESCRIPTION: SEQ ID :237:

5 CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG 50  
ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA 100  
CAGTTTTCCA GCAGTTTTCG TATTNTTTT TATTACGAA TGCCATACTC 150  
10 TGT TTT 156

## (2) INFORMATION FOR SEQ ID :238:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :238:

GCAGNCTAAT TGTGAATCTA AGAACTACT CATAGACATC CCACCCTAAT 50  
25 GATTTTACCT NNAACNTTGG TCCTTCATCA TAGAACCCTA GCAACATCCA 100  
CCTCCTGTAG CACGAAACGA ATCAACAAC CCCCTGGATA ACCTCTCA 148

## 30 (2) INFORMATION FOR SEQ ID :239:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :239:

GAGTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA 50

134

AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA 100  
AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA 150  
5 TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTT TCCACTAAGG 200  
CCCTTTTCT TTTCTAGNT CCCACAGAGG ATACATTACA TTTACTTACA 250  
TCTTCTCT 258

10

(2) INFORMATION FOR SEQ ID :240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA 50  
25 CAAACCAAGT ATTCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG 100  
GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA 150  
CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT 200  
30 TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG 250  
CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC 300  
35 AAGGGTNAAC NTNTTNNAA ANNGCCNAA NCNNGATTTT GNACNCCCTT 350  
TNNCATTGGC ATTNANTGAA AAAAGTT 377

40

(2) INFORMATION FOR SEQ ID :241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

135

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

GGNGCACTGN TCCGAGAGCT TTTTNTCTG AAGAATAGCA TCTTTAATGA 50  
10 GTGTNCTAAT CCTTGTATC TGAAGTTTGG AAATATATTT CCCAGGGTCA 100  
GAACAATACA GAGA 114

15 (2) INFORMATION FOR SEQ ID :242:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :242:

CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTNN CCATTAAAAA 50  
GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA 100  
30 AAAAAANCNA AAGNGGGCCC CC 122

(2) INFORMATION FOR SEQ ID :243:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

136

## (xi) SEQUENCE DESCRIPTION: SEQ ID :243:

5 GAGAATGGGA AGCCTCATTT TGGGGACAAG AACCTGTACA AGGATTGTG 50  
ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC 100  
NTATGATATG CCTCATGATA TTNTTGCATC TGAAGATGGG ACTNTGTACA 150  
TTGGNGATGC TCATCCAAAC C 171

## (2) INFORMATION FOR SEQ ID :244:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :244:

AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT 50  
25 TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAAA GTTAAACAG 100  
GACTTTCAAC TTAATCCAGA CTCCTAACA GTGTTTACAT GTGAGGGAAA 150  
CTCCTTTAAG TAATGCGTAG TGTITTATTT TTACCATCAT TGGNGACAAA 200  
30 AAAAACAAAA ACATAAACAT CTNANGTGAA ATATA 235

## (2) INFORMATION FOR SEQ ID :245:

35

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

137

## (xi) SEQUENCE DESCRIPTION: SEQ ID :245:

GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG 50  
5 TCTAAGTTAA AAACGCCCTG CCCCCTTCTC GCAGGCCACC TACACCGTNN 100  
TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCTGC 150  
NTNTACNTCT AACCNATAA TNACNGCGGC CACCTACTCA TGCCCTANTG 200  
10 CAGCNCACCC T 211

## (2) INFORMATION FOR SEQ ID :246:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :246:

25 GGCTGAGAAT CCTTGAGCTT ACCATTGAT ATTTCTATAT TATTTAAGAA 50  
AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT 100  
ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT 150  
30 GAACATGGTG GTACCTTAGG NATTTCCCTT TNCNATGAA TATA 194

## (2) INFORMATION FOR SEQ ID :247:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

	-----	GGCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
5		GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
		CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
		GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
10		-----	
		GGCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT	249

(2) INFORMATION FOR SEQ ID :248:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 248 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :248:

25	-----	GGCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
		GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
		CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
30		GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
		GGCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC	248

35 (2) INFORMATION FOR SEQ ID :249:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 82 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear



139

## (xi) SEQUENCE DESCRIPTION: SEQ ID :249:

5 GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTGCGGTTG 50  
GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA 82

## (2) INFORMATION FOR SEQ ID :250:

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20 GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG 50  
TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAAACCAGN 100  
GAGAGATGCA CAAGATTTAC AGGCC 125

25

## (2) INFORMATION FOR SEQ ID :251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :251:

GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG 50  
40 AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAA AGCGCGTTTT 100  
TCTGGGGGAG CGGCCGCCTT TAGTCGACCC 130

140

## (2) INFORMATION FOR SEQ ID :252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :252:

GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA 50  
AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT 100  
TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT 150  
ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGGTTTT 200  
ATGNGATAAT ATCAGC 216

## (2) INFORMATION FOR SEQ ID :253:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :253:

GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAAATT 50  
ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTCCTT CCAAGAAGN 100  
TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAGC ATTAAAAATA 150  
TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT 200

141

TTTTCAGAAG GATCTTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT

249

## (2) INFORMATION FOR SEQ ID :254:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15 GACCCCATTC TATATTATNC GTNNNGCGAT TTTTAGCCA CCCTGAAGTT 50

ATATTTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCTNG 100

GAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG 150

20

CTCCCTGGGN TTCTTG 166

## (2) INFORMATION FOR SEQ ID :255:

## 25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35 CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTTCAA GAGCATCTGG 50

AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA 100

AGATTTGCTC GCTGAGAAAG TCCTTGTTGG AAATCGAAGT TGAGGACTAC 150

40

TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC 200

142

CTTCTNTTGT NACAGACAGC AGA

223

## (2) INFORMATION FOR SEQ ID :256:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15	GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AACAGCTCT	50
	TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC	100
	TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA	150
20	CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC	200
	CTGACGATCT TTCCCTAGAT CATTCTGACC TGTGTAGAG TTGTTGAAGG	250
25	AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC	292

## (2) INFORMATION FOR SEQ ID :257:

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :257:

40	AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT	50
	AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG	100

143

ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT 150

GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCACT TTCCTGACGA 200

5 TCTTCCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT 238

## (2) INFORMATION FOR SEQ ID :258:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :258:

GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA 50

20

GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG 100

AACCGGCTCC AAGCATTCTG CACAGCACTA ATTTAAA 137

25

## (2) INFORMATION FOR SEQ ID :259:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :259:

GCGCGACTTT TAAGGGATTG GCNGTGATGC CTGTTGACCC AGTGCCTTCC 50

TAGCCGGGAA GGGGCTCGGC TGGAGTGNN AAGGCTCAGAA AAATTTCGCG 100

40

AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

144

TTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTT CGTGTTACAT 200  
CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTTT AAGGGATTG CNGTGATGCC TGTGACCCA GTGCCTTCCT 50  
AGCCGGGGAA GGGGCTCGGC TGGAGTGNA AAGGCTCAGA AAAATTGCG 100  
20 AAGAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150  
TTTTGGACAG GTGGGGCGGT GACCTTGGA TGTATTTTTC GTGTTACATC 200  
25 GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50  
40 CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT 100

145

ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC 150

ACTTCCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT 200

5 GATCCCTGGA TAAACAGGAT CATTTCAAAG NNGTTTATA 239

(2) INFORMATION FOR SEQ ID :262:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 143 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :262:

GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTGTGTA AACAGCCATT 50

20 GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG 100

TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA 143

25 (2) INFORMATION FOR SEQ ID :263:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :263:

GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCTGTAA TACCTCCTCC 50

TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC 100

40

TAAAAAATA TAGCAATCCA GATAGGCTTC GATTTCCTGT GACACTCTGA 150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT 200

TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT 50

CTGTGTTAAA TCGTATGCTT TTAAAGGTA TTAAAGATT CAACTAGCTT 100

20 TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG 150

ACCTGATCTT GATGTTCTGC TGTTGTNAGT CTGAAGAGC GTATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT 50

TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA 100

40 AAACAGCTGC CTCGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150



147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGTGCCC TCCAAACAGG 200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGGAAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG 50

TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACGCG CGTTGTCATC 100

TCCCAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC 150

40 AGGGTGGAGG CAGATGTCT 169

148

## (2) INFORMATION FOR SEQ ID :268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GTCATCCTA GAAGGGGGGG CTGACTGCAG 50  
GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG 100  
CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT 150  
ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAACA AGTGCTGCCT 200

## (2) INFORMATION FOR SEQ ID :269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG 50  
ATAGCAGCAG CTGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC 100  
TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCTT GAATTGTAAA 150  
CACTAAGTGT AGT 163

## (2) INFORMATION FOR SEQ ID :270:

149

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :270:

10

TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG 50

GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA 100

15

CCTATTATTC TTTCT 115

## (2) INFORMATION FOR SEQ ID :271:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :271:

30

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50

GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN 100

NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150

35

TGCAGAAATN CCTATGTGAC TCTTATAA 178

## (2) INFORMATION FOR SEQ ID :272:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50

GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN 100

10 NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150

TGCAGAAATN CCTATGTGAC TCTTATAA 178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGAAGAA GATCAGAACA 50

AAAAATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG 100

30 CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC 135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40 (D) TOPOLOGY: linear

151

## (xi) SEQUENCE DESCRIPTION: SEQ ID :274:

5 TGTCGAGGAG AAGAAACCAC TTGATAACAC CCCGCGACAT CGTGGGGCTG 50  
CTTGTACAN GAAAGCACCA TGTCGCAAT GGATTGCTGC AGGTGCTGCC 100  
GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA 150  
TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTTCTTCAT 200  
10 GACATAGGTG AGCAGTTTCC AGTCCCACTC C 231

## (2) INFORMATION FOR SEQ ID :275:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25 TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC 50  
TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA 100  
GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTGNNG 150  
30 NCGTNCCCAC CATTGATTGA 170

## (2) INFORMATION FOR SEQ ID :276:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 315 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

152

## (xi) SEQUENCE DESCRIPTION: SEQ ID :276:

ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA 50  
5 ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG 100  
AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC 150  
CTGAGGGAAA CTAATCTGGA TTCCTCCCT CTGGTTGATA CCCACTCAAA 200  
10 AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA 250  
ACGAAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT 300  
15 AGCGTAGCAT ATTNA 315

## (2) INFORMATION FOR SEQ ID :277:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :277:

ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTTGAGA TTTCACAAGC 50  
30 AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC 100  
ATAGTTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT 150  
35 AGCAGAAATA GGCCCTTTTCG TGNGCTGTTT TATTNCTCG GATNGTAGAT 200  
ATAGTAATC 209

## (2) INFORMATION FOR SEQ ID :278:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

153

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :278:

AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC 50  
10 TGCTGTAAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA 100  
GAGTCTT 107

## 15 (2) INFORMATION FOR SEQ ID :279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :279:

ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA 50  
CAGTGCAATA GGCTCCAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT 100  
30 ACTACTGCTT TAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG 150  
TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC 200  
35 GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCNCT ATAAGTGCAC 250  
AAAGGGGAAA CACTGATTTC AAGCTT 276

## (2) INFORMATION FOR SEQ ID :280:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs

154

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :280:

AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA 50  
10 CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT 100  
TAAAAACGC AGAACTTATT TTATCCGTGC TTAGAAATA ACTGTATACA 150  
15 GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT 185

(2) INFORMATION FOR SEQ ID :281:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :281:

AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA 50  
30 CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT 100  
TAAAAACGC AGAACTTATT TTATCCGTGC TTAGAAATA ACTGTATACA 150  
35 GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA 186

(2) INFORMATION FOR SEQ ID :282:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



155

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

TGTGGGCTCA	GTAATGTCCC	CGCTGATGAC	AATTCGAGA	GTCCATGTTT	50
TATAGAAACC	TTGAGGTCGG	CCAGCCGTGT	CTTGGCCAAT	GAGATGTAGT	100
TGTGAGGAGG	GGGCGTACTT	GGGGACCAGG	GGTGGGTGGA	GATGTGCCCT	150
GTAGGCACAG	GGAGACTCAA	AAGCACCAGT	TNTGAAAGCG	TAAATGGG	198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

AGAAAAAGGT	GAAGCGAAGC	CCAAGGACAC	CATGCTAAGG	GCAAAAGTAA	50
GAGACAGTCT	CAGAACTGAG	AGAATCGTGT	CTTCTGCTTT	TTGAAGTAGA	100
CTGTCACACT	CAGGCAGCCT	GTCAATGCTG	AATGTTAGGA	CTTCTGTCTC	150
CGCTGGAGAC	ACGCCTGGGC	AAGTCAGCGT	TTAGTGTTTG	ACAGCTTTCT	200
CAGCTCCCTG	ACTCCGTTTA	CC			222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA 50  
ATGTGNGACG ACACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA 100  
CCTTTGNCGC TGTNTGCA ACGTTCGAG TGNTACTCTG CGTGAACCGG 150  
TAGACTGCTT GG 162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC AAAGCCCACT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA 50  
GACAGCAGAC TCGAGCC 67

30

(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

157

GGTCGGATCA GGTCAACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA 50  
GGCAGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT 100  
5 TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA 150  
GAA 153

## (2) INFORMATION FOR SEQ ID :287:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20

TACTACGGCT AAGGAGAAAC AATGTTCTTA CATATCACGG GTAGTGAGAA 50  
CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT 100  
25 CCATCGTGCT TTAGAAATAA CTGTATACAG TGTTATAAGT TGAAAAGAAC 150  
TCAAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG 200  
CTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC 250  
30 GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC 293

## (2) INFORMATION FOR SEQ ID :288:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

158

## (xi) SEQUENCE DESCRIPTION: SEQ ID :288:

AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT 50  
5 CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC 100  
GTGTTGAATC ACTG 114

## (2) INFORMATION FOR SEQ ID :289:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20

ATGAACCACT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTGCTGGA 50  
AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC 100  
25 CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC 150  
GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC 200  
AGCGTCCGGG AGCCTCCCTG TCCTTGTTGTG GGGTATGGNG CTCTGGCGTT 250  
30 GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT 290

## (2) INFORMATION FOR SEQ ID :290:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

159

## (xi) SEQUENCE DESCRIPTION: SEQ ID :290:

AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50  
5 NACTTTGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG 100  
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTTACTT TTGCTACTGT 150  
TTTGTAGAAC GATGTACATG AATGAGCCT 179

10

## (2) INFORMATION FOR SEQ ID :291:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :291:

TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG 50  
25 TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCTGT AACTCTGCTT 100  
CTGTGGGATT CTGCCCAAGA GATCTCATTA CAGTTCCCAA TTCTTTGTTG 150  
TTATAGTACC ATCACCATTT CGTTAAATAG TGAAAGAGCT TTTTGAATC 199

30

## (2) INFORMATION FOR SEQ ID :292:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

GGAAGACCAT TCTGATCATC CTCACTGACG CCAAGGCAA GAGGGTGGTT 50  
TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT 100  
5 CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC 150  
AACCGAANNG ATATTACAAT GTAAAAA 177

## (2) INFORMATION FOR SEQ ID :293:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20

ATTGGTTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA 50  
CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC 100  
25 AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT 150  
TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACCTTGN GTCTGTTTCT 200  
TTTAGGCTCT TTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC 250  
30 CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GGCCT 295

## (2) INFORMATION FOR SEQ ID :294:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

161

## (xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG 50  
5 CATATTTTAC CATTTTGNA AACTGTGAG 78

## (2) INFORMATION FOR SEQ ID :295:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :295:

ATTCTGTACC TGTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATTT 50  
20 GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG 100  
GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTGAGA 150  
25 GAGCCCGGTA ATA 163

## (2) INFORMATION FOR SEQ ID :296:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :296:

AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC 50  
40 CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA 100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT 150

CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCCTC 189

5 (2) INFORMATION FOR SEQ ID :297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCTGAAC TTCCTGTCCC CACTCACACA 50

AGTGGTCCGG TGTCACCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT 100

20 GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150

GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG 50

CTCTGGAGAA ACAAGTTGTT CTGTGAGGCC CTGCCCATCA ACACACTAAG 100

40 CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150



163

GTATCATCAT GCTGCCTCCT GCATTGAAT T

181

## (2) INFORMATION FOR SEQ ID :299:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15 AACATTGTTT ATTCATCCAG CAGTGTGCT CAGCTCCTAC CTCTGTGCCA 50  
GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTtagc ACAGCCTGGG 100  
GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA 150  
20 CTGCAAGCTG CTTGCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT 200  
CATCTGGTTG TGA CTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT 250  
TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC 300  
GAGGCATGTA CATT 314

## (2) INFORMATION FOR SEQ ID :300:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :300:

40

AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC 50

164

CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT 100  
TTTAAGAACT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA 150  
5 AAGGAGAGAC AAGTGCAA 168

## (2) INFORMATION FOR SEQ ID :301:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :301:

ACCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG 50  
20 GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG 100  
CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT 142

25

## (2) INFORMATION FOR SEQ ID :302:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :302:

AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCCT 50  
GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG 100  
40 AGGCCCCACAA GGACTCTCAT TGAGTTCTTA CTTGTTTCA GTCAAGACAA 150

165-----

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG

197

## (2) INFORMATION FOR SEQ ID :303:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15 AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT 50  
GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC 100  
CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA 150  
20 TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT 200  
AAAAGTTTTT GAATAAATGA TGAAAATTTT TTAAC 236

## 25 (2) INFORMATION FOR SEQ ID :304:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 220 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :304:

ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC 50  
CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG 100  
40 TCTAGCACAG CCACCGCCCC CATGCCCAGG CTCAGGAGCA CACTGAGGTC 150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200

TTAGGCCTCC CGTACAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA 50

ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAGNTC 100

20 AACCTTCGAT GCTATCCCC AGCCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNG 100

NGNTGATATA AACAGATNNA 120

40

(2) INFORMATION FOR SEQ ID :307:

167

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100

15

NGNTGATATA AACAGATNNA 120

## (2) INFORMATION FOR SEQ ID :308:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :308:

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTATCAT 50

30

AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA 100

GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC 150

35

TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG 200

AGCCGGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG 247

## (2) INFORMATION FOR SEQ ID :309:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

168

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG 50  
AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT 100  
ATGCCGTT 107

15 (2) INFORMATION FOR SEQ ID :310:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG 50  
ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG 100  
TATCAGGAAA GAGA 114

30

(2) INFORMATION FOR SEQ ID :311:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

169

## (xi) SEQUENCE DESCRIPTION: SEQ ID :311:

ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC 50  
5 TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT 100  
TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC 150  
GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA 200  
10 GTTGTCAATA CCACCTCCGT AGCCCCCACC CTGTTGC 237

## (2) INFORMATION FOR SEQ ID :312:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25 TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG 50  
TGGTGACAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA 100  
GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC 147

30

## (2) INFORMATION FOR SEQ ID :313:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 151 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG 50

CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA 100

5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG 150

G 151

(2) INFORMATION FOR SEQ ID :314:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :314:

20

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC 50

AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA 100

25 AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT 150

TATCACTAGG CTAAACTGG ACAAAGACCG CAAAAGATC CTCGAACGGA 200

AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA 250

30

ACCATTGACA AGATGAGGAA TAAGTAATTN ATATANA 287

(2) INFORMATION FOR SEQ ID :315:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear



171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

50  
GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT  
5 GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTTCA 100  
CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT 150  
GTAAACTAAG GTAGACTACT CTGNGAATAA GAA 183

10

(2) INFORMATION FOR SEQ ID :316:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :316:

50  
GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTTCA AAAACGTGGG  
25 TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100  
CCACCTTTGC AGCCTGTTTC TGTCATGTAG TTTCA 135

30

(2) INFORMATION FOR SEQ ID :317:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :317:

CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC 50

172

TGCCGAAGTC CAAAAGCTTC AGCATTTTCCT TAGTGTGAGG ATCTACTTCA 100

ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC 150

5 CTATNTTTTC TGGGGCTTGA TGGAGATACC TTTACTG 187

(2) INFORMATION FOR SEQ ID :318:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :318:

TCCCAGGAGA AGGAACTTTG AAATTCATCC CAACGTAGGC TGAGTGACCT 50

20

GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTGAGCATT TCCTTAGTGT 100

CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA 150

25

ATGCTCTCCT CCCTTNCCTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT 200

GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN 250

AGCTTTCNGT TGNNTAA 268

30

(2) INFORMATION FOR SEQ ID :319:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA 50

AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA 100

5 GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT 138

## (2) INFORMATION FOR SEQ ID :320:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :320:

AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTTC ATAAACCTCA 50

20

GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT 100

GTAATCATAC TTCCCCCA 118

25

## (2) INFORMATION FOR SEQ ID :321:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG 50

GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC 100

40

GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT 150

174

TTCCTTTTCC

160

## (2) INFORMATION FOR SEQ ID :322:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :322:

15 AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCCC 50  
AACAGGGCTG CTGATTGTTT CTTTCACTTT TGNGGTGACC TTGAGCTCCC 100  
TTAAAAA AAAA AACTTGGAGA ATCACAACG GCAATGCACC GCAGTTCTCG 150  
20 AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT 200  
GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA 250  
25 ACCCCCTGGG AGTATAATNN TCTCCATANA A 281

## (2) INFORMATION FOR SEQ ID :323:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :323:

40 GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50  
ANTTTATNNN GTCTTCTTA ANNTAGAGTG ACTTACTGAT TTATTATTG 99

175

## (2) INFORMATION FOR SEQ ID :324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50  
ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA 100  
CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA 150  
TTGCCCGCGT TTTTAGG 167

20

## (2) INFORMATION FOR SEQ ID :325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAACCT CTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA 50  
AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG 100  
ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCCTCTT 150  
TCGGGTCGCG 160

40

## (2) INFORMATION FOR SEQ ID :326:

176

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10

GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT 50

GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG 100

15

AACATGAGAG AGCAGAGTGC TCTC 124

## (2) INFORMATION FOR SEQ ID :327:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :327:

AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA 50

30

GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT 100

CGACAATGTA ACTCTGCAAA TCGATGGAGT CCTTTACCTG CCATCATGGA 150

35

CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG 200

CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA 250

AGT 253

40

## (2) INFORMATION FOR SEQ ID :328:

177

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :328:

GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA 50  
TAGAAGAAGC TCAGTATCGG CTCCTCCCAC CATAACCGCG TTNAATCGC 100  
CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCATG CTCCTGCTAC 150  
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTAT 200

## (2) INFORMATION FOR SEQ ID :329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :329:

TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC 50  
TCTTTCTTTT NTCGAAAATN ATAAACTGC GTATTCTACT TTATATTTAA 100  
TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG 150  
AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA 200  
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA 250  
GGATTACCAA CTCCTGCTG CCATGACCGA 280

178

## (2) INFORMATION FOR SEQ ID :330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CCTGAAAAAC TTTATGGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTTNT	50
CGAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA	100
AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT	150
TCATATGTTC ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC	200
AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT	250
CACTGCTGCC ATGACCGA	268

## (2) INFORMATION FOR SEQ ID :331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT	50
AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN	100
TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC	150



179

TACCATATGC CCTTAAAAAT

170

## (2) INFORMATION FOR SEQ ID :332:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15 TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50  
AGAGTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100  
TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150  
20 TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGTTTCTGT 200  
GTTCCAAAAA TTAAGATTG GTT 223

## 25 (2) INFORMATION FOR SEQ ID :333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAATCCCA CAAGTTCTTC 50  
TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG 100  
40 TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC 132

180

## (2) INFORMATION FOR SEQ ID :334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC 50  
15 TGAATAACC AGTGCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT 100  
CCATNTTTC CAATTCAAT TGTTGGGAT TCTAGCACTC CTTACCNGCA 150  
GTAATGCCCT TGCTGCAGAC AACAACACCT GGA CTGNGAG ATGGACCAAT 200  
20 TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT 235

## (2) INFORMATION FOR SEQ ID :335:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :335:

35 ATGCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50  
ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC TCAAGTTCGA 100  
CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG 150  
40 GNGATCACCA ACAGGAGAG 169

181

## (2) INFORMATION FOR SEQ ID :336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCCGAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50  
ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC TCAAGTTCGA 100  
CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG 150  
GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG 193

## (2) INFORMATION FOR SEQ ID :337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC 50  
TCAGGGTCTT TGGATTGTTA CCAAAGCTG TCAAACAGAC CAGTAGTTTA 100  
ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG 150  
CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT 200  
CATCTGCAGG ATTCCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCAA 250

182

AAAGGCAAAC TAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG 300

CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CACAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50

CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTTAA 100

20 TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150

TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200

25 ATCTGCAGGA TTCCAGCTT TGCTCAGTCT TCATGCCCAC CAGAGGCAAA 250

AAGGCAAAC TAAACTGTCA TGCAGTGGTA GGTGAAAT NAGCTGCTGC 300

30 ATCAT 305

(2) INFORMATION FOR SEQ ID :339:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA 50

ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG 100

5 G 101

## (2) INFORMATION FOR SEQ ID :340:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :340:

GTCGCAGGAG AAAAAAGTCG TCACGTCATG CGAGTGC GCA GGGGGCGTGG 50

20 AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA 100

AGGACTTCCC GCA 113

## 25 (2) INFORMATION FOR SEQ ID :341:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :341:

ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAAAGCAAT 50

ATAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC 100

40

AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA 150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200

TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

TTTtagacag GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100

20 GCTTTTAATC TTCATTTTNN NNTTTTGTTA TGGTAGGCTG AGATGCTTTT 150

AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200

25 TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250

TA 252

30 (2) INFORMATION FOR SEQ ID :343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :343:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100  
GCTTTTAATC TTCATTTTNN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150  
5 AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200  
TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250  
TACAAAAC 258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC 50  
25 CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG 100  
ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA 150  
TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG 200  
30 CACAGGACCC AGGAGTCCGC CCACCTG 227

(2) INFORMATION FOR SEQ ID :345:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

186

## (xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50  
 5 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100  
 CTGGCACACT ACTAAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT 150  
 CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA 188

10

## (2) INFORMATION FOR SEQ ID :346:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 262 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :346:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50  
 25 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100  
 CTGGCACACT ACTAAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT 150  
 CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT 200  
 30 NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC 250  
 TAGAAGTGNA AA 262

35

## (2) INFORMATION FOR SEQ ID :347:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



187

## (xi) SEQUENCE DESCRIPTION: SEQ ID :347:

5 CTCTGTTTTT CAAACGCCCA TGTGTGCTAT ACTACAACTC TTCTCGAGTC 50  
TGATCAATTT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC 100  
ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTAAAAGA 150  
10 AATNTCTAA 159

## (2) INFORMATION FOR SEQ ID :348:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :348:

TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC 50  
25 ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCGTGATC AATAACATCT 100  
ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC 150  
30 CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC 200  
TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA 250  
TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC 283

35

## (2) INFORMATION FOR SEQ ID :349:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5 CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AACNGTGGA 50  
CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC 100  
GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG 150  
10 TGGATCACCC AGGTCAGGA 169

## (2) INFORMATION FOR SEQ ID :350:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25 GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC 50  
AACCCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT 100  
GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA 150  
30 CTTGGCAACA NCACAGGAAG GGACC 175

## (2) INFORMATION FOR SEQ ID :351:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

189

## (xi) SEQUENCE DESCRIPTION: SEQ ID :351:

AAATAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA 50  
5 AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG 100  
GCACACTACT AACTGTAAAT GTTTTAAAT TGAATCTGTA AAATTGTAA 150  
GGTTTATGA ATATAATATT ATTAATATT ATGTCTCTGA ATTTTNNNN 200  
10 NAGGCT 206

## (2) INFORMATION FOR SEQ ID :352:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25 AGACATACTG TAGTGTCTAA ATAATATTG TCNGAAGATA ACAATTATGG 50  
GACTTTAAAG CCGACAGTGA AATTAT 76

## (2) INFORMATION FOR SEQ ID :353:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40 ACATTGGGCC CTCAGACTGT AATTCCATA CTACTNTGAC TGATACTAGA 50

190

TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAAA 100

ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG 150

5 GGCCTGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC 200

GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA 245

(2) INFORMATION FOR SEQ ID :354:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20

GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC 50

AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG 100

25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT 150

CTTTGGGTTG AGACTTTTCA GNGACAACT 179

(2) INFORMATION FOR SEQ ID :355:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40

AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC 50

191

TCCAGCATGT TGTCAACCATT TCAACAGAAA TCGCACAAAT GCTACTGTGC 100

AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG 139

5 (2) INFORMATION FOR SEQ ID :356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAACTTC CACTTATAAC TGTNTCAGCC TGACTATAAT 50

GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT 100

20

(2) INFORMATION FOR SEQ ID :357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGA AGACTAACCA 50

35 AGATTTGGAC ATTGGAATGT TTAAGTTAT TCTTTAAGAA ACAACTACAA 100

AAAGAAAATG TCAACAAATT TTTCTAGCT AACTGAG 137

(2) INFORMATION FOR SEQ ID :358:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

192

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :358:

10

AAGGAACAAG TGGGTCATTC TCACTAAGGC TGCCTGTCAC TGCAGTCTTG	50
ATCAGCTTGT CAATTTGATA CTTACAGCTTT TGGTCCAAGG GACGAAGCTT	100
TTCCAAAACC GTTCGAATCT CTACCACTCT CAAAACCTGCA TCATGTCCCT	150
GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG	200
GGNACATGAG CAGCAGCTGN TCTTTAAC	228

15

(2) INFORMATION FOR SEQ ID :359:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :359:

30

CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT	50
CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA	100
CACTCACCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA	150
CCAAGAAAAT GAATAAAACA GCCAACTCG ACCTTCTTAT GCAGAAAATT	200
GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC	248

40

(2) INFORMATION FOR SEQ ID :360:

193

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :360:

10

AGGCACCTGT GGAGCCATCC TCCTTGTTTT AATCGTCCTG CTGCTGCTGC 50

CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC 100

15

TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA 150

CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT 200

GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT 250

20

GCC 253

## (2) INFORMATION FOR SEQ ID :361:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :361:

35

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50

GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100

CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150

40

TAAT 154

194

## (2) INFORMATION FOR SEQ ID :362:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50  
GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100  
CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150  
TAATCCTGNC CACGCCCT 168

20

## (2) INFORMATION FOR SEQ ID :363:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA AGGAAGCTTT GNCACCACTC TACCATCAAA NNGGAATTGA 50  
ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAAA CATGNATTTT 100  
ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT 150  
CTCTCTATTT NTTTCTCTGG TTGTCGACCA GCTGACTNTG NCATCGTT 198

40

## (2) INFORMATION FOR SEQ ID :364:



195

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGA AGGTCATAGT AAGCATACCT ATGCTGAGAG 50

AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC 100

15

TCGTACACTT TCAAGTTTAA A 121

## (2) INFORMATION FOR SEQ ID :365:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :365:

30

GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA 50

AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAGAGTT TTCAATGCTT 100

TCTAAAAGTT TCCTCTTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC 150

35

GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT 200

CTCCAAGGGA G 211

## (2) INFORMATION FOR SEQ ID :366:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

196

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT 50  
GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC 100  
ACTGTCAGGA GAATGNCCCC TGTCGAATCA TCGATCTCCA TCCGAGCCAA 150  
AAGTTTTCCA TATGCTGAAA TTAAGAATT GCCCTCGTTT ATAGTATATG 200  
ATACAGTGGC CTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT 250  
TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG 285

20

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :367:

GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG 50  
GTCTTGGCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA 100  
ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT 149

35

(2) INFORMATION FOR SEQ ID :368:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG 50  
10 CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTGTG CCTCGCTGAG 100  
GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG 137

## 15 (2) INFORMATION FOR SEQ ID :369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :369:-----

GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTTATTTT CTGTTAGTGA 50  
CATGTAGTCC CTTTGTCTA GTAGAAAAA AGGTGCCTAG AGGTAGTATA 100  
30 TAGAGTAAAT ATTGTTCTT TGCCTACTCG TGCTTCCAAT GATTAAGGAA 150  
ATGTTAAACA NNNGTNAAG TCTGTTTTGT CAATGCGGGA GT 192

## 35 (2) INFORMATION FOR SEQ ID :370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

198

## (xi) SEQUENCE DESCRIPTION: SEQ ID :370:

5 GAGACTTAAG TAAAACGGCT GCAGGCCAGA TCGCCCACC AGCTCAGAGA 50  
CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT 100  
GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTCACGNAT 150  
10 ATAGTAGAAA CCAAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAT 197

## (2) INFORMATION FOR SEQ ID :371:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC 50  
25 ATACACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC 100  
GGGCTTTGGA GAGG 114

## 30 (2) INFORMATION FOR SEQ ID :372:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCTCCACA TTCCCTTCAG 50

199

CTCCTAGTTG TTCCACCTTG GCTAACAAATT TACCAATCTT TTTTCTATG 100

AACACGTTCT GCCTTGCTG CTA~~CT~~CTC 127

5 (2) INFORMATION FOR SEQ ID :373:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTC 50

TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCCCTTA CTCAGTAGCA 100

20 GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT 150

TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG 200

25 CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT 250

TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

200

NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT 100  
CCGTGGGAAT CACTGTCTGA GTCTGTGTC TAGTATTGAC AGATATAGCT 150  
5 TTGTTCTTGG AGTAGAATTA AGGAATTGCG 180

## (2) INFORMATION FOR SEQ ID :375:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :375:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGTT 50  
20 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC 100  
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150  
25 TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAAC ATCTTACTGA 200  
TGCTTACTTC AAGAAGAAGA AGCTGCGGAA GCCCAGACAC CAGGAAGGTG 250  
AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA 300  
30 TTGATCAGAA AGCTGTGGAC TTA 323

## (2) INFORMATION FOR SEQ ID :376:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

201

## (xi) SEQUENCE DESCRIPTION: SEQ ID :376:

GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTTT CTAAGAGGTG 50  
5 AAATCACTCG CTGGTGTTTA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT 100  
ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTCACAG 150  
ATGGGGGGTA GTTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG 200  
10 AGTCAGTCCT GCATTATGT CTT 223

## (2) INFORMATION FOR SEQ ID :377:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25 GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTTCCC 50  
CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTTGTGTCAT 100  
ATGGCTAATC AAGAGCCAGG TA 122

30

## (2) INFORMATION FOR SEQ ID :378:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

GGCAGTGCCT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC 50  
TACAAGGTGG ATAATACTTC GGTACCTTGC TGCCACAGC CCTGTTCTC 100  
5 AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA 150  
AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT 195

## (2) INFORMATION FOR SEQ ID :379:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :379:

20

GTAGCCCTGA GGTATCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG 50  
GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACTTG GAAGGTTATA 100  
25 GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN 150  
GGTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT 200  
ATANNNNNGG 210

30

## (2) INFORMATION FOR SEQ ID :380:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :380:



203

CTGGCTCACC TGGACAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT 50  
GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA 100  
5 ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA 150  
CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG 200  
GCCACAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA 238

10

(2) INFORMATION FOR SEQ ID :381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :381:

GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA 50  
25 ATAGCTGTTC ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT 100  
CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAAC 150  
GATTGGAAAT CTTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA 200  
30 AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAACAGG TGGAAGAAAA 250  
CCTAGCNCGC ACAGAACATA AGCTC 275

35

(2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5 AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCAGCCCA ACACTTTAAA 50  
CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA 96

## (2) INFORMATION FOR SEQ ID :383:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20 GGAATTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA 50  
AGGAGCTCTG GGCACCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC 100  
TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT 150  
25 CAATNCNAAT NGANNGGTTA CTCAAAGGG ACGAGACATG CACCTG 196

## (2) INFORMATION FOR SEQ ID :384:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40 AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC 50  
ATTTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA 100

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG 150

CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT 200

5 CCCCAT 206

(2) INFORMATION FOR SEQ ID :385:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :385:

GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTTAC 50

20 CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG 100

AAGCCTGGGG NCACCTAGGT GTTCTATTA TAAA 134

25 (2) INFORMATION FOR SEQ ID :386:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :386:

CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC 50

40 ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA 100

CCAGGACGCC ACGCCGACGA ACAAGGGGAG TTCNGAGGAG GAGGAGGCCA 150

206

GGACGAGGCG T

161

## (2) INFORMATION FOR SEQ ID :387:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :387:

15 GGTGAGCCTC CGCCATCCAG CCAAC TGTGC GAC CGCAGCTGTG 50  
CCGTGGCAG ATGGCGAGGA AGCCAGCCCC AAGGACAC TGAAAACACA 100  
ACCAGTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGTT 150  
20 GTTTTTTNAG GCAGTAATNT 170

## (2) INFORMATION FOR SEQ ID :388:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :388:

35 TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50  
GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100  
GCCCAATACA AAATACACAG AAAAAGCAAT TATTAATAAC GGCTTCGGTT 150  
40 TCTTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC 200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTC AACTGAAATC — 250

## (2) INFORMATION FOR SEQ ID :389:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15 GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCTTCCT 50  
CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT 100  
CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN 150  
20 TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG 200  
AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC 250  
25 GTAGGGCNTG AGGGAGGT 268

## (2) INFORMATION FOR SEQ ID :390:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :390:

40 GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA 50  
GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT 100

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG 150

CCAGGTATAC ACCTTANAGA GGATGAC 177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA 50

TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG 100

20 GCAACCCCAA AACACCTCT TNCTGNCTGC CTCTGCAA 139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC 50

TATCTGGGGC GCCTGGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC 100

AGCCACCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA 150

40 AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCGGAG 200

209

AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCACGGA CTCCTGGTCT 250

GAGCCCAAT 259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGAAG GTACTGGTCC AATTATCTA GGAAGTATCT 50

CTTGAGTTT CAGAAATGCT AGCTTGACA ACTGAAAAGT CACATCACAG 100

20 CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG 150

GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC 189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA 50

AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AACAGA 97

40

(2) INFORMATION FOR SEQ ID :395:

210

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10 AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTT 50  
GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC 100  
15 CCCTTGACTG ATTTATTGTC GTCAAAGCA TGTCCTCTA TCTTTNNNN 150  
TCACGATC CGCTGCCTTT CTACATCTGA GAATCTGTC AAGCATGGAT 200  
AAACTTGNTT TTATGTTGCA TATTTTACG GCTTCAACTT GAGT 244

## (2) INFORMATION FOR SEQ ID :396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT 50  
35 TTTTATTCTG ATCTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA 100  
GCTTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA 150  
TTGCAGCCTT TCTTTTCCGT TTCTTTTNTG AAGGG 185

## (2) INFORMATION FOR SEQ ID :397:



211

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :397:

10 GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG 50  
CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG 100  
15 AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC 150  
ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTGTCTGA 200  
ACACTGCTTA TCTGACCC 218

## (2) INFORMATION FOR SEQ ID :398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :398:

30 GGAAGCAAAA AAACAAAAC TAACTCGAAT TTGCTTCCAA ACCTGTAGAT 50  
35 TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC 100  
CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAAT 150  
GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATTT GACCCAGAA 200  
40 AACCCAGTA CCTTTNACA ATGACCCAAC CANTACCTAC CATCGGCCAG 250

212

## (2) INFORMATION FOR SEQ ID :399:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :399:

TCACCTTGATT CATCCGTCGC GGGATTGGG AGCACTAGCA ACATAATCAA 50  
CACACTCCTA CAATCTTAGG CTTACATGT GCTGATGATG ATGAAACCAA 100  
CTCTGCCCCA ATCATCTCCC CTTCTNNTAG GGTCTTACTA CATATCGCAA 150  
CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCACTACCC 200  
TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA 250  
ATAATGAGAT TAAATTTATG TTTCGAGT 278

## (2) INFORMATION FOR SEQ ID :400:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :400:

GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA 50  
GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA 100  
GCAAGCTCTC TTCCTTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTTA 150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA 200

ATGTGTT 207

5 (2) INFORMATION FOR SEQ ID :401:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA 50

GGGGGCCAGC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC 100

20 AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC 150

AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG 200

25 NTTCTCCAAA GATAGCC 217

(2) INFORMATION FOR SEQ ID :402:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTTACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT 50

40 CTTCCACAC TCGCACATCG AAACATTTTT GTGCCAGGGC TTTCCAGCTC 100

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCACATCT GGAACACTTC 150  
TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTTTGG ATTTGTTGTA 200  
5 GGCCTGTGAG GCTGAACACT CTCTG 225

## (2) INFORMATION FOR SEQ ID :403:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG 50  
20 ACTGNGGCTT CCACTGCGCC CGTGACNTT ATCGAAGCTA CAGAT 95

## (2) INFORMATION FOR SEQ ID :404:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :404:

35 AGGAAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG 50  
CAAATTCCAA AACAGAAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG 100  
GGCCACACTG TGTAATACTG TGCCAACTTA TGCGAGTCTC ATTGTTTCAGG 150  
40 ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATACC 200

215

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG

239

## (2) INFORMATION FOR SEQ ID :405:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15 GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA 50  
TGTCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG 100  
AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA 150  
20 GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC 189

## (2) INFORMATION FOR SEQ ID :406:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35 CACCATCCTC CAAGTAAATC CCCCTTAGG AAAGTAAGGG AAAAGACCCC 50  
TTATAGCCCT GAGCTCCCCC TTGGA 75

## (2) INFORMATION FOR SEQ ID :407:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 190 base pairs

216

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :407:

10 TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT 50  
TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT 100  
CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG 150  
15 CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC 190

## (2) INFORMATION FOR SEQ ID :408:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :408:

30 GAAGACATGG CGCCCTAACA CTCGAGACC TGCTGNTAAA TAAAAGCTA 50  
TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG 100  
CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG 150  
35 CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT 194

## (2) INFORMATION FOR SEQ ID :409:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

217

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATT TAACCACTTC 50

TAAACAAGA TCATCTTCTG CAGCACCTGG TTTTAGTTTA TCCTTGA 97

10

(2) INFORMATION FOR SEQ ID :410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCTTC TTTGCCTACA CTGGCCTTCC TCTCGGAGGG 50

25

ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNTNTG GTCCAGGGCC 100

AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC 150

TTTGC 155

30

(2) INFORMATION FOR SEQ ID :411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA 50  
AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC 100  
5 TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG 150  
TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA 200  
TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT 249

10

(2) INFORMATION FOR SEQ ID :412:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 143 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCAGC 50  
25 TTTACTCCTC TATAACTCAT CTTACACCCN GCATATTAA ACAAACTAAC 100  
AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT 143

30

(2) INFORMATION FOR SEQ ID :413:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCC ATTACGTAC TCCATCACAA AGTACAGGCG GTCCATGGTC 50



219

TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA 100  
CACCCACTTC TCCACCATAG TGCACTCCAC GTCATCATCT GATCACAACG 150  
5 TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT 200  
GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT 250  
AAAATC 256

10

(2) INFORMATION FOR SEQ ID :414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :414:

TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA 50  
25 GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC 87

(2) INFORMATION FOR SEQ ID :415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :415:

AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT 50  
40 TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCGCCCGC 100

220

GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC 150  
ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG 200  
5 CAGTGTTCCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC 247

## (2) INFORMATION FOR SEQ ID :416:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :416:

TCTAGCACAC AGCTGCGCTC ACAAAACTG CGCGACTTGT TAGAACTAAT 50  
20 TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA 100  
TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATT 150  
25 ACATTGAAAG GA 162

## (2) INFORMATION FOR SEQ ID :417:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :417:

CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTAA 50  
40 GTACTTAGCA AAATATTTGT TTNCGTGAT TTAGCTTGTC ATTAAACNAA 100

221

GAGCTACTG

109

## (2) INFORMATION FOR SEQ ID :418:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15 GGATGTAAAT TATATGTTGT TTAAATTTT CCAGCATCTG AAAACCTTAT 50  
CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTT 100  
TAAATAGTAC ATATCATTAA ACCATTCNTT CTAAANGTAA GAAGAGCAGA 150  
20 AAAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA 200  
AA 202

## 25 (2) INFORMATION FOR SEQ ID :419:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC 50  
ACCACAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACAG 100  
40 CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC 150

222

TA

152

## (2) INFORMATION FOR SEQ ID :420:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15 CAGCCCTACA CTCGCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA 50  
TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA 100  
AGATCAATGC CCTCATTAAG GCAGCCGGTG TAAATGTTGA GCCTTTTTGG 150  
20 CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT 200  
CTGCAATGTA GGGGCCGG 218

## 25 (2) INFORMATION FOR SEQ ID :421:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAACT CCCCCACCCA 50  
GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCTGGT CCCTGGAGTC 100  
40 CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC 150

223

TGCTGGCTGT CCTATGCCAG CTCACCCAT GTGGGGACCA CGNAAGGCAC 200

ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA 237

5 (2) INFORMATION FOR SEQ ID :422:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGNGTAATA AATACTGCAT CCTTCCACA ACATAGCAGG AATCTTATAG 50

GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG 100

20 TTTCTTTACG AAGTGAAAT AAGTGCTGCA CCATACTGTA AACAAACTC 150

GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT 200

25 CC 202

(2) INFORMATION FOR SEQ ID :423:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG 50

40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA 100

224

TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAAT 150

ACTGACTTCG GTTCTTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA 200

5 TTCGTATCAG CACCTA 216

## (2) INFORMATION FOR SEQ ID :424:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :424:

CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT 50

20 GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCATA TGTCCCTCGC 100

CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG 150

25 GGTGCCCTTT TAAAAAAA 168

## (2) INFORMATION FOR SEQ ID :425:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :425:

TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGTTAC 50

40 TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA 100

225

GAGGAGTCAC AGTGGAACCT CCCAGCTTTA AGATATCTAG CAGAAACTAT 150  
AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG 200  
5 GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC 250  
TAATTAGG 258

(2) INFORMATION FOR SEQ ID :426:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20

TCCACATCAT CTCCAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG 50  
CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN 100  
25 GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC 150  
CATGCACGAA GGAATTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCACG 200  
CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTTGTGCC AGCTGCTGTT 250  
30 CGAATNNTTT TCTTTCTCGT AAAGC 275

(2) INFORMATION FOR SEQ ID :427:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

226

## (xi) SEQUENCE DESCRIPTION: SEQ ID :427:

CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA 50  
5 GAAGCCGAGA GGCAAATGT CATCATATGC ATTTNTGGC AAAGTGTGG 100  
GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT 150  
CTAAGAGTGC TC 162

10

## (2) INFORMATION FOR SEQ ID :428:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 220 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :428:

ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC 50  
25 CCATAGTTCC TGAATCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC 100  
TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA 150  
GTCGNGTTTA CAATGATTG NCCTGGACTG AAATTCANGC TGCCTTAAGG 200  
30 TGCTGATGAT ATTGAGAAGT 220

## (2) INFORMATION FOR SEQ ID :429:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40



227

## (xi) SEQUENCE DESCRIPTION: SEQ ID :429:

5 GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA 50  
GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT 100  
GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG 150  
GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA 185

## (2) INFORMATION FOR SEQ ID :430:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 277 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :430:

GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC 50  
25 TACCTGGTCG TGGGAGTAGT GGTGATCGTG GACCCAGGGG TGATCCCTAT 100  
CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC 150  
TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG 200  
30 GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG 250  
GAAGACACCG CAGAGCTCAC TTACCAA 277

35

## (2) INFORMATION FOR SEQ ID :431:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

228

## (xi) SEQUENCE DESCRIPTION: SEQ ID :431:

5 AAAGTGGCGCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGGCTGGTC 50  
GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT 100  
CAGCAAGGAG GAAGAAGTCA TTGTT 125

## 10 (2) INFORMATION FOR SEQ ID :432:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT 50  
TCGAAATAGC ACATTTTTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA 100  
25 GACTGATATT CTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150  
AATCCCCC TTTATAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200  
30 ANAANGGAAA TGGGGCAGGA CA 222

## (2) INFORMATION FOR SEQ ID :433:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :433:

229

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50  
CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100  
5 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150  
TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200  
NGNCGTTTCC TCT 213

10

(2) INFORMATION FOR SEQ ID :434:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :434:

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50  
25 CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100  
CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150  
TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200  
30 NGNCGTTTCC TCTGCCGGTG T 221

(2) INFORMATION FOR SEQ ID :435:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT 50  
5 TAGTATATTT TCGTTGTCAG 70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT 50  
20 CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA 100  
GACTGATTGA GTACAAAATG AAAGTGTGCG TCAGCTTGAT CCATTTTGTC 150  
-- 25 ACCCTCAAGT AGG 163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA 50  
40 AGAAGAAACA GAGGACAAAA AAACAGACGT TAAGGAAGAA GATAAATCCA 100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150

CTCAGCAACC CCTGAATTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50

AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100

20 GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAAGTGTGT 150

AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTTCGAGA AACAAATAGTG TATGTGTTCC TATAGGTATG 50

AGTTATTGAN TGTAGATTCTG TTTTCTGCA ATCCTCTGCC GAAATGATNT 100

40 ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA 200

CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTCAG CTTTCCAGTT GACACCAAGT 50

CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA 100

20 CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200

25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50

40 TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

233

ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT 150  
GGAATAGGCT TATTAAGTTA CACATTTAAA AAGTCATTAG AACATCTCGT 200  
5 TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT 250  
GGTT 254

## (2) INFORMATION FOR SEQ ID :442:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50  
CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100  
25 CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC 147

## (2) INFORMATION FOR SEQ ID :443:

## (i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :443:

40

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50  
CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100

234

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC 150

TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT 198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTCCTACA TATTATGGGT AGTGAGACAT 50

TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTC 100

20 TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA 150

AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT 200

25 TTCTGTGA 208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTTC ACTACGGGNT ATGTGCATTG TGGGCTTAGT AATGTCAAAT 50

40 CACTCTTCTC TCCAGCTTGG CCATTCTCTA TTCCTTGC GGCTGCCCTG 100



235

TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCTGTAA 150

CCTGNAGCCC CCGCTGAG 168

5 (2) INFORMATION FOR SEQ ID :446:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCGTGATT GGTGGATAAA 50

GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA 100

20 TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA 150

AGGAAGCCAT GTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA 200

25 CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA 243

(2) INFORMATION FOR SEQ ID :447:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAT GATTGCCAC CTGTTTGTAGA 50

40 AATCTAAAT NNTAAGTAAC TAAGAGCAA GTGCTATGTG GGTTTTAGAC 100

236

CATGACTGTT TGTTCCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG 150  
CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GTGCTCTGG 200  
5 GGAGGAGAGA GGAGAGAACA GGCTGTTTTG GAAATATCC AGCACTTTGA 250  
C 251

## (2) INFORMATION FOR SEQ ID :448:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20

ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNGCAGGA ACGTGATGGC 50  
AACAAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAACATAT 100  
25 ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAAATAA GTTTTATAGT 150  
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA 200  
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA 250  
30 GTG 253

## (2) INFORMATION FOR SEQ ID :449:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA 50  
5 ATACCTCTGT AAGAAGCAGA ATACACCATA TGTATTAC ATGTATAGGA 100  
GTGATAAGAA AAT 113

(2) INFORMATION FOR SEQ ID :450:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

20

TAGCATCCAG GGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA 50  
GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA 100  
25 AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG 150  
AAACTATTTG AGATCAAAGT CCTATAACA AAGTTAAATG ATTCCAAGAG 200  
GTAAATAGGA G 211

30

(2) INFORMATION FOR SEQ ID :451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

238

CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG 50  
NATTTACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTTNTCTG 100  
5 TAGAATGATA TGGCCTGATA TGGAGGCCCTC TTAATNGGCT TTTTCAAGCA 150  
GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG 194

(2) INFORMATION FOR SEQ ID :452:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA 50  
TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT 100  
25 TAAAACTACT TGAATTCTA CTCATAATA GGAGTCAGTC ACTTCTGGGA 150  
CTATAGTGAT GCTTGCAA 168

(2) INFORMATION FOR SEQ ID :453:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCAGAC GTGAACCAAT 50

239

TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTG CCCCCTTCAC 100  
TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA 150  
5 TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA 200  
TAGGACGCCA GACTACACTG 220

## (2) INFORMATION FOR SEQ ID :454:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20

GCCATCCTTG ATGGAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA 50  
AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT 100  
25 TGCTTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT 150  
ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTCAA 200  
ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA 250  
30 TAGTTTGTGCT TTGTCTTTAG CGGTT 275

## (2) INFORMATION FOR SEQ ID :455:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

240

## (xi) SEQUENCE DESCRIPTION: SEQ ID :455:

TCGCAGAAGG AGGAACGGGG ACTTTCATC CCCTGAACCA AGGCATGTTA 50  
5 AACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG 100  
CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGAATTCCTT 150  
AACANNTATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTTTG 200  
10 TTAACACCGA CAATTAGTTG TTTACACCC AGTGGTAAGC CAGAAGGGCA 250  
TGCTCTNGGG TCTGCCCAT 270

## 15 (2) INFORMATION FOR SEQ ID :456:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC 50  
ACGACCCCTG CGCTGGATAC GCGACGGTT TCTCATTTG CCTTGCCAG 100  
30 CTCTCATTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT 150  
TTCTTAAGGA GCAAACAGC TTCCTGNNC TTCTGTAGC CTCAACTTA 200  
35 TTTAACTAC CAAGGAAGTT CAGGAAGTTC CTCAANACGA TGACCTTTAG 250  
ACAT 254

## (2) INFORMATION FOR SEQ ID :457:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

241

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :457:

ACACTA	ACTG	TTCCAT	CCGT	TATATT	TGCT	GTGAGG	AAAA	TTAAGAT	TCC	50
10	TGTTGT	TATGG	GCTGCA	CTGT	TTCTGG	AAGA	CTACAG	AAAA	TCTAAC	100
	TATGG									
	TTGACA	CTTC	CTGGTA	GCCC	TTCTGT	ACAT	ACACAC	ACAC	AACCAAG	150
15	GAAGAC	CAGAG	AGAAAAT	CCT	GGTCCAA	AAG	ATCACAT	GAC	CTTACTAG	200
	TG									
	TTTCCCA	AT	GACTGT	AATT	TATAAA	CTAA	AAATTG			236

## (2) INFORMATION FOR SEQ ID :458:

20

## (i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	108 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	double
25	(D)	TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :458:

30

GAGANN	NNNT	NNGGNA	AATG	NTNCGC	ACT	GNAGCT	AAGA	ANAGNN	ATGG	50
NNNTAG	GGNG	NNAGAN	GNCN	TGAAC	AGAGA	AAGCNT	GAGG	GCTCTG	GGGAC	100
35	GCTGGT	AT								108

## (2) INFORMATION FOR SEQ ID :459:

## (i) SEQUENCE CHARACTERISTICS:

40	(A)	LENGTH:	155 base pairs
	(B)	TYPE:	nucleic acid
	(C)	STRANDEDNESS:	double

242

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC 50  
CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC 100  
10 CCATGTTCTT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA 150  
GAGGT 155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC 50  
CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT 100  
30 CTGGTTTGTG GAGGTTTACA GACATGTGTT AGTATATCCT TGCCTGCATG 150  
TAGTTGTTCA TTACTAGAC 169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



243

## (xi) SEQUENCE DESCRIPTION: SEQ ID :461:

5 ACCNTGTTTA ATTANTGCCG GGGCTCGCCG TTTGCATACA ATGGCTTACT 50  
CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT 100  
TTTATCAGCG TACCTTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG 150  
10 GCTTAGGGCA TCGAAAAACC TAAAGTCGA GCTT 184

## (2) INFORMATION FOR SEQ ID :462:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :462:

25 AGGAACCN TG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT 50  
TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA 100  
GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA 150  
30 GGCGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN 200  
AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTCGGCCGT 250  
NNACTGNGTT GTTGGCGACA GATGT 275

35

## (2) INFORMATION FOR SEQ ID :463:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

244

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5      AATTCATAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA      50  
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT      100  
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGNGCCA GCAATGCTA      149

10

(2) INFORMATION FOR SEQ ID :464:

(i) SEQUENCE CHARACTERISTICS:

15      (A) LENGTH: 179 base pairs  
         (B) TYPE: nucleic acid  
         (C) STRANDEDNESS: double  
         (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :464:

ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT      50  
25      CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT      100  
GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG      150  
CCCAAGTCAC ACAGCTAGTG AAGACCAGA      179

30

(2) INFORMATION FOR SEQ ID :465:

(i) SEQUENCE CHARACTERISTICS:

35      (A) LENGTH: 156 base pairs  
         (B) TYPE: nucleic acid  
         (C) STRANDEDNESS: double  
         (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :465:

245

CTACCTCTGT GCCAGGGCAG CATTTCATA TCCAAGATCA ATCCCTCTC 50  
TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA 100  
5 GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA 150  
CCAGAG 156

## (2) INFORMATION FOR SEQ ID :466:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA 50  
CTGCTGGTTC TGGTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC 100  
25 TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGCCTCACC 150  
ACTCCCCTNT GTCCCCCAG CAGGGGGACA AAACAG 186

## (2) INFORMATION FOR SEQ ID :467:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

TNNNGATGAN TATANAAGCA TCATNGACGG TATTTCCTCNG TCTTGNANTT 50

246

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

## (2) INFORMATION FOR SEQ ID :468:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15 ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA 50  
TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTTGCCTGG TATTGTGTTG 100  
AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT 150  
20 AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA 187

## (2) INFORMATION FOR SEQ ID :469:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35 AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA 50  
GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GTCAAAAAG TTCAACCTTT 100  
GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA 150  
40 ACATCGGCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA 200

247

GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA 250

ACTGAA 256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT 50

GAAGTCTGAA TGGAGCCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA 100

20 GAGGGTTTG 109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAACTTT ATCAATCATA 50

GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTTGC TTGNAGACCT 100

ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTCT 139

40

(2) INFORMATION FOR SEQ ID :472:

248

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10

TCGCAGGAGA AGGAATGTTT CCAATAGGAA CGCCTGTAGA CTGTTTCAGAA 50  
GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG 100  
GCTCTGAGGA CTATAGATTT ATCCTCTAGG TGATGAGGGA CTATTAACGG 150  
CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTCACGT 200  
GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA 250  
TGGGAGACAT TT 262

15

20

## (2) INFORMATION FOR SEQ ID :473:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35

ACAGAAGGAC TTTGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC 50  
GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT 100  
GCATCTCTCA TACTTNNATC AGCCAACATG AACACTCTAT GTATTTTCTA 150  
AGCTTTCNTC TGTTCAAGAA CTTTGAATTT AAAACGTCT 189

40

249

## (2) INFORMATION FOR SEQ ID :474:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACCTAA ACTCGAACGC ACGTAATAGT GCTCATAATT 50  
CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGA CTCTAGC 100  
AGCCTCGCTA ACCTAGTTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT 150  
GTTAGTACGC GNGTTA 166

20

## (2) INFORMATION FOR SEQ ID :475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT 50  
TCCTTCAAAA CTGTGTTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT 100  
TCAACTTAA 109

40

## (2) INFORMATION FOR SEQ ID :476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

250

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi). SEQUENCE DESCRIPTION: SEQ ID :476:

10 TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA 50  
GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA 100  
CGGGTCACTC AGTTACGTTT AGCCACAGCC T 131

15 (2) INFORMATION FOR SEQ ID :477:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :477:

ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCTTAC 50  
ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100  
30 TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC 150  
AGTGTTATAA GTTGAAAAGA ACTCAAATA ACTAATACAA ATATACACTA 200  
CGTATTAGAA TTCAAAAAG CTGCTTTCTG TGAAGTCAAT CAGCTATATT 250  
AAAAAAGACA CAAAT 265

40 (2) INFORMATION FOR SEQ ID :478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs



251

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :478:

AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAGACC 50  
10 TGTNTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTGT 100  
ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT 150  
15 NTTTCATCATG GTGTTGTCTA GGTCTCCTGA GG 182

## (2) INFORMATION FOR SEQ ID :479:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :479:

AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAAACCA 50  
30 CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA 100  
AACGGGAGCC TCTAAATCTT GGTGGGACT GCTCGCCTGG AGCCGCACTC 150  
35 TTGAGTCCGA GGCCATCTT 169

## (2) INFORMATION FOR SEQ ID :480:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

252

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT 50  
CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTTCTGTC TCACCGGATA 100  
10 TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATT AACAGACCCT 150  
GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA 200  
15 ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC 238

(2) INFORMATION FOR SEQ ID :481:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC 50  
30 TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCCGAA GTCTGCAAGC 100  
AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG 150  
35 ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCCTGT CTGAGGGAGG 200  
C 201

(2) INFORMATION FOR SEQ ID :482:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

253

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

CGGCTCAGNC TGTTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
ACNTTTTTAG AT	162

15

(2) INFORMATION FOR SEQ ID :483:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACNT NCCTGAACCT	150
GAGGGAAACT TTGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAACT	250

35

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs

254

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

10 AACATTATCT TGACAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG 50  
AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG 100  
ATTAGAATGT TAATGCCACT TTGATTAGAT CT 132

15 (2) INFORMATION FOR SEQ ID :485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :485:

TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC 50  
CGCATTCACG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC 100  
30 ACGGACTTCT CGACACCATC AAGAGCGAC 129

(2) INFORMATION FOR SEQ ID :486:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

255

## (xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG 50  
5 AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG 100  
ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT 150  
CATTGCACTT CAACCATATC GA 172  
10

## (2) INFORMATION FOR SEQ ID :487:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210-base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAACTAAAT GGATCCATTA AAAGTTATGA 50  
25 TTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA 100  
TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC 150  
AGCACTCCTC TATGGGCACA GACACACACA CAAATTTGTC CTTGCTTTTC 200  
30 TCAGATATAT 210

## (2) INFORMATION FOR SEQ ID :488:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50  
5 ANACGTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 99 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA 50  
20 TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG 50  
CCCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC 100  
TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150  
40 GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCC GA 186

257

## (2) INFORMATION FOR SEQ ID :491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :491:

AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA 50  
ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT 100  
TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT 150  
GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG 200  
CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC 250  
TTCATATCGG AAA 263

25

## (2) INFORMATION FOR SEQ ID :492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :492:

AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT 50  
AAATNGGTGT GGGNGGTCCG CTTTGGCCA TCATCGCACC CCCCCGGTCA 100  
CTGGGCGTTG TTGCCGGGCA CTTGTTTNNC NGGCTGGGTG TGTACCGTAA 150

258

CCGTGGGTC

159

## (2) INFORMATION FOR SEQ ID :493:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15 GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGGA 50  
CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT 100  
CAAATCAAGG TATCGGGAAG AATAATTTCC CCTCGATTCC ACAGGAGGGA 150  
20 AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT 197

## (2) INFORMATION FOR SEQ ID :494:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35 GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA 50  
GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC 100  
CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG 150  
40 GGAGGGCTGC TGTGAGTGGA GTCTTGAGTN GGTGACTG 188



259

## (2) INFORMATION FOR SEQ ID :495:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTATTGAC AATGAGAAGA TGGAGTCCCG	50
GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTGCCACG AGAGTGAGAC	100
GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT	150
GTGGGNGCTG CTGGGGAGG	169

20

## (2) INFORMATION FOR SEQ ID :496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTCTATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG	50
AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGAAGTCCC	100
ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC	150
TTTAAACCGT CAAGCTGGGT GG	172

40

## (2) INFORMATION FOR SEQ ID :497:

260

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :497:

10

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCTCCAG 50  
TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCCGGTC 100  
ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA 150  
ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCACCCC TTAGGGTGTG 200  
TNTCATCGAA GTGTAGNGAA TGGTGAACG TTTGTTTGTN GTGTGC 246

20

## (2) INFORMATION FOR SEQ ID :498:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :498:

35

GCCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT 50  
CTGGGAGACT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG 100  
CCACTATTTT TGTTGTATAT CTTCACTCTCA ATGGCGACAT GGCCACTGCC 150  
CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT 200  
GAACATCGTG CGTTA 215

40

261

## (2) INFORMATION FOR SEQ ID :499:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT 50  
AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCTGTTC 100  
ACANGAAAAT AAAGCTAGGG AGGTGATTGA TCTATCCGAG AAAAAAGCCG 150  
GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT 195

20

## (2) INFORMATION FOR SEQ ID :500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT 50  
GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAAATG CTTTCAACAA 100  
ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG 150  
TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG 200  
CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG 250

40

262

GTGGAGCTGT

260

## (2) INFORMATION FOR SEQ ID :501:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15	AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT	50
	TAAATNCGTT GCTACAAAGT GTTTTGTTC TCTAAAAAGT AGTTTTGCA	100
	TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTGCT TTATATACAA	150
20	CAGTTAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA	200
	CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA	250
25	ACCATGGCTT GCCCAAAT	268

## (2) INFORMATION FOR SEQ ID :502:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :502:

40	AAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG	50
	GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC	100

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA 150

CC 152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC 50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA 100

20 NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T 141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC 50

GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG 100

GCCGAGC 107

40

(2) INFORMATION FOR SEQ ID :505:

264

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10

ACCCTCTTCT GATAAATTG AGGGCCCGTT TGTCTTGA GACCTTCAGT 50

AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT 100

15 GTCCCGCAGC AACTTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG 150

CTGGGCTTGC TCACGTTCTT GTCACTTTGT GGCCCTTGTT GAG 193

## (2) INFORMATION FOR SEQ ID :506:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30

ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTTCCTACA 50

TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100

35 TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT 150

GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT 200

TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250

40

TGACACAAAT CCAAACAAGA TGCA 274

265

## (2) INFORMATION FOR SEQ ID :507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :507:

	CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA	50
15	AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA	100
	GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCAGCA	150
	AGTGTTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA	200
20	CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA	250
	CCATTGAGAA GATGCAGGAG TAAAGTATTA T	281

## 25 (2) INFORMATION FOR SEQ ID :508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :508:

	AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG	50
	CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA	100
40	GCAGAGGGGA CAGAGATGAT GACCCCTTCG CTCCTCCCTG CAAATGAGCC	150

266

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

180

(2) INFORMATION FOR SEQ ID :509:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

15 AAATGCAAAA CTCACCGTGC AACTCCTAG ATCCCTGCCA CAAAGAAATC 50  
TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT 100  
ATTT 104

20

(2) INFORMATION FOR SEQ ID :510:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG 50  
35 GGAAGCTAGA GCCAGAATCA GGAAAATCTG TTCCTCGTC CCCAGACTCC 100  
CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA 150  
GACTTGCATC TGNATCTTGN A 171

40

(2) INFORMATION FOR SEQ ID :511:



267

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10 ACTGTACCTA TCATCCTGAA AAACCTTTATG GGGGAGAAAG GTCAGCAGCT 50  
TCTCTTTCTT TTNATCGAAA ATAATAAAAC TGCGTATTCT ACTTTAACTA 100  
15 AATGTAAGGA AGAAAATATA CAAGCCCATATA TTTAATGTAT TTCTATNCGA 150  
GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT 200  
GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG 250  
20 GATTA 255

## (2) INFORMATION FOR SEQ ID :512:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :512:

35 GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT 50  
TTCTTGCTTT ATTTGTGACA TTTCAGTTTA TTAGAAATCA TGTTACCATT 100  
AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTGATTT GTGTAACCTG 150  
40 ATAAAAGATT TACTGACTTA AGCTTTTGTT TTTTTCATA AGCTGCTTTT 200

268

GAGCTTTGTC

210

## (2) INFORMATION FOR SEQ ID :513:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15 CTGTACAATC ATCCTGCAGA AAATGTTTT GGAGAATTCT TGGTAATTGA 50  
AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG 100  
AACAGGGATT CTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAA 150  
20 AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG 200  
AAGAAACAAA CGTGTGCATC CT 222

## 25 (2) INFORMATION FOR SEQ ID :514:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT 50  
GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC 100  
40 AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA 150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACTCT TAAACCTCAT AGCNAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA 50

ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA 100

20 TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATAACACG 100

40 AACACTCATA CACACANGCT TGTGCACACA TGTTTCATGCA CATGCATGCA 150

270

CTCACACTCA TACAAACGCA CATTAAACA CGTGTGNACA NTGTACTCAG 200

ACACACACAG GTGTG 215

5 (2) INFORMATION FOR SEQ ID :517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA 50

GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG 100

20 TGTCGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC 150

AATCATGGGC CCTAGCCGNC CTNGTAATAC G 181

25 (2) INFORMATION FOR SEQ ID :518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTAACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT 50

GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT 100

40 AGCCAATATA GAAGACGTGT GCCTCACAGG GTTCACTTTG TTCATCAATA 150

271

AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT 200  
CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA 250  
5 CCTGGCAACT 260

## (2) INFORMATION FOR SEQ ID :519:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :519:

AAGCTAATAC AATGGTCATT TCCAGACAAA TTAAAGGAA AACTAAGGC 50  
20 TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA 100  
CATGCTCTTT TTTTA 115

## 25 (2) INFORMATION FOR SEQ ID :520:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :520:

CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTGCGAGA 50  
AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA 100  
40 CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT 150

272

GACTNATAGN TNGACCCACC TGTGA

175

(2) INFORMATION FOR SEQ ID :521:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15 ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT 50  
TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100  
TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA 136

20

(2) INFORMATION FOR SEQ ID :522:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :522:

AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG 50  
35 GATATATTTT GTGTCTTCTG TGA CTGTTCA TTCATGGAAG GAAGCAGACT 100  
GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC 150  
TATTCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC 200

40

(2) INFORMATION FOR SEQ ID :523:

273

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :523:

10

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT 50

CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA 100

15 CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC 150

ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA 200

CATA 204

20

## (2) INFORMATION FOR SEQ ID :524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT 50

35 GGCAACAAGT GCAGGTTTTT TGGCTTTCTT TGATTCATAT TGTGCAAGAC 100

GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA 150

GAGGTCAATG TATCATCA 168

40

## (2) INFORMATION FOR SEQ ID :525:

274

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :525:

10

AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT 50

AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTG TCCTTTCTCA 100

15

GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC 150

ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT 200

TTATCTCCCT CTGCATTCAG ACCAGGCTCC TTAGTGCACT CATCAGACTA 250

20

TCGCTGCCCC TGCTGTCTGC TGTGAGCCT TCACCACCAC T 291

## (2) INFORMATION FOR SEQ ID :526:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :526:

35

CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAACTCA 50

TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC 100

CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG 150

40

AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT 200



275

GGGAAGC

207

## (2) INFORMATION FOR SEQ ID :527:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15 AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC 50  
AGGTCTAGGG AGGTGTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC 100  
CCAGCCAGAC TACATTTCTT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC 150  
20 CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC 200  
CTCTGACCCA GCTTCACC 218

## 25 (2) INFORMATION FOR SEQ ID :528:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

AACCTNATGA CTCTCCATCC CTTGAACCA AACATCTAGC ACTCAGCTCC 50  
AGCATATTTC ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT 100  
40 GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC 150

276

CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT 200

TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGCCA 50

ACAAGTGCAG GTTTTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100

20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50

GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT 100

AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA 150

40 TATGCACATG CTGGTGCTAC CCTCTCACT 179

277

## (2) INFORMATION FOR SEQ ID :531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAT ATCTTCTCAG 50  
CATTCAAAC AAAACGCATA AGTCATTCTT AACTTNAGAG CTTTATAGCA 100  
TTTTCCTAGA CAGGAAGGGA AAAACAGTT AGCATTTAA AGTCCGGAAA 150  
GCTTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTTG TCCAAATCCC 200  
TTAT 204

## (2) INFORMATION FOR SEQ ID :532:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :532:

AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC 50  
CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC 100  
CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTAAAATACC 150  
CTTCTTCAA AACTTAGCTC TGAATGGAGA AAC 183

278

## (2) INFORMATION FOR SEQ ID :533:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :533:

GAAACAAGTT CTCGCTCATC CCTGCATTTC TGCCAACTTC AGCTTGCAAT 50  
ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC 100  
TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG 150  
TTTACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG 200  
GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT 250  
AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT 287

## 25 (2) INFORMATION FOR SEQ ID :534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :534:

AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT 50  
GACTTTTTC AGTCAGTTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG 100  
GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT 150

279

TTAG

154

## (2) INFORMATION FOR SEQ ID :535:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15 GATTACCCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG 50  
GGCCTATTTC TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA 100  
TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG 150  
20 GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC 200  
CTAGGAAGGC AC 212

## 25 (2) INFORMATION FOR SEQ ID :536:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

GGAAGCTCAA TGTCGGCAG GTCAATGCTT CNCGGACACG GATCATTTTT 50  
ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC 100  
40 CTGCCCCCTG GGAAGGNACA GTGATGTCTT TAGGGGAAGG AGGAGCCCCT 150

280

NTCGGCAGTT GTCTTACT

168

## (2) INFORMATION FOR SEQ ID :537:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15 CGGATCATT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT 50  
GTTCCCTGCT GCCTGCCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGGAA 100  
GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNTAA TGAAGTA 147

20

## (2) INFORMATION FOR SEQ ID :538:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :538:

GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG 50  
35 GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT 100  
GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT 150  
GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA 200  
40 AATNAATGTA AACCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC 250

281

## (2) INFORMATION FOR SEQ ID :539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :539:

AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT 50  
GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTCGGGG ATGGTGAATG 100  
CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC 150  
CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGGC 184

20

## (2) INFORMATION FOR SEQ ID :540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :540:

AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTA 50  
CCAGGGAAGT CACCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT 100  
CATCATCATG TCTCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC 150  
AGAT 154

40

## (2) INFORMATION FOR SEQ ID :541:

282

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA 50

ATTTTGTTTT CTTCTGTGTT ATTGGTTCAA AGTACTGGCC TTTCCTTCA 100

15

TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA 150

TGATTGCTT ATACTGTGAA ACAGC 175

## (2) INFORMATION FOR SEQ ID :542:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT 50

CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC 100

35

AGCCGTGCTG CTTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT 150

GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG 200

AATCGCGACT GGCNAACAGA T 221

40

## (2) INFORMATION FOR SEQ ID :543:



283

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :543:

10

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG 50

GAGAAACATA CCTTGAGAGG GGGTTTCTT TAAAACTAGT GTTAGAAGCT 100

15

TAGGGATTTT TTTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA 150

TTTGACTTGT GCCGACATTG CAACTTTNT GACAGG 186

## (2) INFORMATION FOR SEQ ID :544:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :544:

30

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCTGCCT 50

TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA 100

35

CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT 150

GCC 153

## (2) INFORMATION FOR SEQ ID :545:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs

284

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :545:

GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG	50
TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT	100
ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG	150
CCCAGGCCTG T	161

15

(2) INFORMATION FOR SEQ ID :546:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :546:

AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA	50
GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAAC TGAAGGTCA	100
TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA	150
TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA	188

35

(2) INFORMATION FOR SEQ ID :547:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTCTG 50  
ACRAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA 100  
10 GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT 150  
TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG 200  
15 AATCACTCAT TTAGAAAA 218

(2) INFORMATION FOR SEQ ID :548:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT 46  
30

(2) INFORMATION FOR SEQ ID :549:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG 50  
TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG 100  
5 AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTCNC 146

## (2) INFORMATION FOR SEQ ID :550:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :550:

AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA 50  
20 ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT 100  
TGACTCTAGT CACCTTGTTG TGCGAGCAAG TACTAGGTCT TATTCATTCT 150  
25 TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA 200  
TTTAAAAAG ACAATGCTAG G 221

## (2) INFORMATION FOR SEQ ID :551:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :551:

40

AAACATCGTT TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC 50

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG 100

GGGAGGGGGT CATTGT 116

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT 50

CAGTATCGCT CCTCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG 100

20 TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT 150

(2) INFORMATION FOR SEQ ID :553:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50

GAGGCGCTAA TCAATAAAAA AAGTTAACA TTTGCATGAC TCTACTATGG 100

GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150

40 NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT 189

288

## (2) INFORMATION FOR SEQ ID :554:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50  
15 GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTGCGATGAC TCTACTATGG 100  
GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150  
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC 198

20

## (2) INFORMATION FOR SEQ ID :555:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAC TGAAGAACTT 50  
35 GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG 97

## (2) INFORMATION FOR SEQ ID :556:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 269 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

289

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

	TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAAACTTCA TCCTCTTGTT	50
	GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA	100
10	GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCTAGG	150
	CTGTTCAAGGT CTTCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT	200
15	CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT	250
	CTTCAAGGGT GATCTTGTT	269

(2) INFORMATION FOR SEQ ID :557:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :557:

30

	ACTCCCTCAA GGTGCGTGGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG	50
	ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT	100
35	GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAAC	150
	AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG	200
	ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC	245

40

(2) INFORMATION FOR SEQ ID :558:

290

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10

GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC 50

ACAACCTTCG TTCCGCAGTT CATTAAATCCG ACTCTGATGC TAAGGTGACA 100

15

GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT 150

GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT 183

## (2) INFORMATION FOR SEQ ID :559:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30

GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG 50

AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA 100

35

TGCTNAAGAA GCTGAC 116

## (2) INFORMATION FOR SEQ ID :560:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



291

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC 50

TGGATACGGC GACGGTTTCT CATTTCCTT TGTCAGCTCT CATTGCTGA 100

10 GAGGCATAGA CCTTTTGTAT ATCATCAGGC TTCCGTTTT TAGGAGCAAA 150

ACAGCTTCTT 160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC 50

AAATGCACCC CGTTCCCCTG TGCGAGATCG TTTGAATNAG ACCAGAACT 100

30 G 101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40 (D) TOPOLOGY: linear

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTGAT 50  
5 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100  
TATGAGGAGT GGAATTTTAG ATGTCTATTA CATNGTCTT TTAAAAGAAA 150  
AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183

10

(2) INFORMATION FOR SEQ ID :563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187-base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :563:

AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC 50  
25 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTCGGTA 100  
AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150  
GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187

30

(2) INFORMATION FOR SEQ ID :564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :564:

293

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA 50  
CACAGAAAAA TGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT 100  
5 GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC 150  
AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC 200  
AANGTGACTA TTC 213

10

(2) INFORMATION FOR SEQ ID :565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :565:

TCCATCTGAC ATCGCATTTT CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50  
25 GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG 100  
CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT 150  
TTCTTTTTTT CCTTTAA 167

30

(2) INFORMATION FOR SEQ ID :566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :566:

294

GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT 50  
GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT 100  
5 TTGTCGATGA ATTGAGCAAC TGAGAACG 128

## (2) INFORMATION FOR SEQ ID :567:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :567:

GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTGGA 50  
20 AAGTAGTCCT CAATCTTCGA TTCCCGAGCA AGGACTTTCT CAGCNAGCGA 100  
TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT 150  
25 GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG 200  
NG 202

## (2) INFORMATION FOR SEQ ID :568:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :568:

ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA 50

295

AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA 100

CGGGTTACTT TCAAGGAAGA GTTGTTTTGT GACAAATTCT ACTCTTGATC 150

5 TA 152

(2) INFORMATION FOR SEQ ID :569:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :569:

CAGGTCCGCG TGCTCTCCGC ACCACCCAC TTCATTCCGG CCAAACCAAC 50

20

CGCACCCCTG AATTTCTCCG CAAATTCCT GCCGGCAAGG TCCCAGCATT 100

TGAGGGGATG ATGGATTCTG TGTGTTGAG AGCAACGCCA TTGCCTATTA 150

25

CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T 181

(2) INFORMATION FOR SEQ ID :570:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :570:

ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT 50

40

AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCCTCNNT 100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA 150

ATGCTTT 157

## 5 (2) INFORMATION FOR SEQ ID :571:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA 50

AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTACCGCT GGCTTTGACC 100

20 AGGGTATGAT CTTTAAC TTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC 150

ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC 193

## 25 (2) INFORMATION FOR SEQ ID :572:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA 50

GAAGGATTG AGGAGGTTGG TGAATTGTT TGAAGGAGAG GGCGAGGAAG 100

40 AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG 150

297

CTTTCCTGTT TTAAACATGA AAGTGTGGC

179

(2) INFORMATION FOR SEQ ID :573:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15 AGGACCTCTA AGACATCCTT ATGACGACAG TTTTGTCCAA GGGGATATCC 50  
ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTAAAAAGA 100  
TTTTATTCT GATCTTTTGG CGATCTTCTT CTGCCCCATG NNGCTGTTAC 150  
20 TTNGCNCGGG NAGCGGTAA TTCTANCCGC TAGGTGTGC 189

(2) INFORMATION FOR SEQ ID :574:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35 GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG 50  
TAAAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CAAAGAATCG 100  
TCCTTTTTTG AACTATAATN CCCNCGGTT ATTTTACCAT CACAGTTTAA 150  
40 ATGTATATCT TTTACGTCTC TACTCAGACC ATATTNAAA GGGGCGCCTC 200

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAGAT CTGAATTTTG 250

GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50

CCTGAC 56

20

(2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT 50

35 CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100

CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT 150

CGTATCTT 158

40

(2) INFORMATION FOR SEQ ID :577:



299

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG 50

GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT 100

15

CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG 150

AGTCTTCCTC CTGGACTTCT GGTCTGGTA GGCTGTGCTT CATGCTCTCC 200

TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA 250

20

CTTTG 255

## (2) INFORMATION FOR SEQ ID :578:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :578:

35

GAGGAGTCCA TGCCATCCTT GATGAAAAG AACTGAAGA GAAAAGACAG 50

CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAGA GAAAATATGA 100

CATGATATCT TTGCTTTTGA GTTCCTCAGC CTCTCTGAAT TTATTAGTTG 150

40

GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC 200

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC 250

TCTTGAGATA GTTTGTTTT 270

5 (2) INFORMATION FOR SEQ ID :579:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA 50

GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC 100

20 TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG 139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA 50

TGTTGATCC AATTTATTTC TTGGATAAGT TTTTCTTTCC TATNCCTNTN 100

GTTTTGATAA TATAATAAAG AAGATGAGGG GCCCA A TATAGAGCTC 150

40 CTGAGNGAGT TTTNGGAG 168

301

## (2) INFORMATION FOR SEQ ID :581:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :581:

	CGGAGGGCCC TGT TTGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA	50
15	TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT	100
	TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC	150
	CATTCTCCCT GGCTGCCAGC CCTGAAGTC AGAACACCAT GGGAAAATTC	200
20	AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA	242

## (2) INFORMATION FOR SEQ ID :582:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :582:

35	GCATTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG	37
----	---	----

## (2) INFORMATION FOR SEQ ID :583:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGG 50

ACAAGAAACA CTTACCAACA AAAATATTTC AACAACCCCA AAATAACTTA 100

10 CTCACAAATA TGCAAAATTA TCTATGGCAT AGTATTTTCG ACTCGATGAC 150

ATTAGAGAT AAAAAATCAA ATGGAGCTT 179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

AACTGCCATG AAGTAACCTG AAGGAGGCGC TGACTGGAGG GATTGATTAC 50

AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA 100

30 GCGGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT 150

TTGCGACCAC AATNCACCCT TCATTTGTA ACTGCT 186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

303

## (xi) SEQUENCE DESCRIPTION: SEQ ID :585:

5 ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAATA AACTACAAAC 50  
GCACTCACAT CGCTATAATC CTTTAAAGGA CTTAAACTTT ACTCCATTAA 100  
GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCCCTATA 150  
10 CCTCGGAGAA CTTTCGCGTA ATAACCACGT 180

## (2) INFORMATION FOR SEQ ID :586:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :586:

25 ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTTG GCTAANNNNN 50  
NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC 100  
TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG 150  
30 AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG 183

## (2) INFORMATION FOR SEQ ID :587:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN 50  
ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA 100  
5 GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT 150  
GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG 200  
NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT 250  
10 GAGACTGATG TGACNTTCCT GGGACTGNCA 280

## (2) INFORMATION FOR SEQ ID :588:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25 GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA 50  
CCCCAAGATG ATTACACTGA AATGTACTAT TAGTACTNCT GCCAGATCTC 100  
TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAAGT GTTAAGCCAC 150  
30 AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATT 200  
TNTTTTGTG CTTTTTGGGG TATTTTCATT AGTATTTTCAG CAAATCTCAT 250  
35 GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG 300  
ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT 350  
GNGNNGCANG CTTANCTATG A 371

40

## (2) INFORMATION FOR SEQ ID :589:

305

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10

GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA 50

TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT 100

15

GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA 150

TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT 184

## (2) INFORMATION FOR SEQ ID :590:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30

GGGGGCCCCG CGTNCACNCC CCCCACTCT TGGTAGGCAA TGCTTGTCCTC 50

NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTTCATG GATANGGTGN 100

35

GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCTTN 150

AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG 200

CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT 243

40

## (2) INFORMATION FOR SEQ ID :591:

306

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10

ATTCGCCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTACTGAGAC 50  
NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN 100  
NAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAACTTT CAAATTCGCG 150  
CCCTTTNGGC NANGCCCAAC CANNCCCCC CCCTTTTNC CGNCCCANNC 200  
TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC 247

20

## (2) INFORMATION FOR SEQ ID :592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :592:

35

GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAAATGC ATACTGTTTG 50  
ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT 100  
CCANGGATTA CGTTGCAATG TCTTCAAAA TAGANAATTC ATTTTATATT 150  
TCTNGATGAA ATATAATAGT ANCTNNGCTA CTTTGGGAA TGTGACAAA 200  
TACTATGATG ATTACAACTC ATTAAAGCAT AAATNTGCAT GATTAACTN 250

40



307

CATGTTCCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA 300  
TTTANGGCNT NNGTGCTTTG TAATGATTG NCNTTAGGTG AAGGGNTACT 350  
5 TTTNTNNTNC TTCNTAGTAG ATTNNGNTNN NTCTTTTAA GAGGANTCNA 400  
NTTTCATGNG TAANCATCAT CTTTT 425

## (2) INFORMATION FOR SEQ ID :593:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20

CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC 50  
GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA 100  
25 CGCGTGTGAA CACATGCGCG CNNGCGGCNC GCGATNCAA GCTGAAATGT 150  
GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAAACAA CAATGAATGA 200  
ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA 250  
30 ANCAAAAG 258

## (2) INFORMATION FOR SEQ ID :594:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

308

## (xi) SEQUENCE DESCRIPTION: SEQ-ID :594:

GACCCTAACA ATATGTACAA AAATATAAAA TGTAATAAAA AAATACAAAC 50  
5 AAATTTTCCTT TTAAAGTAC TTAAAGAAA AAAAGCAGGG CCTTGAAGT 100  
TTGGTTCTT TTTTCCTCCC CTGTGCAAA TTCTCATGGT TTGGGTGGG 150  
TGTTGGAGAG CGCGTGTCTAT CTGCGGGTGC CTGCCACGT GGGCGGGCGG 200  
10 CTCTCTACTC GAAGG 215

## (2) INFORMATION FOR SEQ ID :595:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 272 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :595:

25 GGGGCTGGTT TGGTCATCCG AGATCATTA AAATGGCTGA CCCTAACAAT 50  
ATGTACAAAA ATATAAATG TAAATAAAAA ATACAAACAA ATTCCTTTT 100  
TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTTT 150  
30 TTCCTCCCCT GTTGCAAATT CTCATGGTTT GGGTTGGGTG GTGGAGAGCG 200  
CGTGTCTACT GCGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT 250  
35 CGAAGGTGAC CACGTTTAGA TT 272

## (2) INFORMATION FOR SEQ ID :596:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

309

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

GACAAACTGT TGACACCCGG AGGCCTAAAC GAGGATTTC A GCTTCCATTA 50

TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAAATGAG CTGCTAGTGG 100

10

AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT 150

CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC 200

15

CTTCCTCAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG 250

(2) INFORMATION FOR SEQ ID :597:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA 50

30

AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT 100

ATCAAGAAAC CAGACTGTGA TGA CTGGGAG AGCGGGCTGA ATGCAATGAG 150

35

TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGA ACTGCAC 200

AAACTGGCCA CTGACAAAAA TGACC 225

(2) INFORMATION FOR SEQ ID :598:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

310

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTATAGAT TTTCATTAC 50  
10 AAAAAAAGTC ATTCACATT TACTATAC ACGTTATGAT ATAATACAGG 100  
AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA 150  
15 CGTGTGTTC TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA 200  
CACCAGGGAC 210

20

(2) INFORMATION FOR SEQ ID :599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC 50  
AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT 100  
35 AGAAGTGAAA AAAAAA 116

40

(2) INFORMATION FOR SEQ ID :600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC 50  
CCCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA 100  
TGGCCTC 107

(2) INFORMATION FOR SEQ ID :601:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

25 ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTTAGC CAATGTTACC 50  
GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAGCA CAGAGTGAGT 100  
TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC 150  
30 ATTTTCTTTC CTTAGTGTA CAA 173

(2) INFORMATION FOR SEQ ID :602:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

312

## (xi) SEQUENCE DESCRIPTION: SEQ ID :602:

	GGAAGAGAAC ACATACACGA GGACCAGTAC CTGATGAGGA CAAGAGAGAT	50
5	GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT	100
	CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA	150
	GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC	200
10	AAGTACCCAG TAGGAG	216

## (2) INFORMATION FOR SEQ ID :603:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 213 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25	GAAAAACAA TCATGACAGC AACTCTCCTA ACCACAAAAA TCACATATGT	50
	TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA	100
	TTTCTAGGGC CCTTCTTGGG GAAAGGTCA TATAATTTAG CATACATACA	150
30	TATTCAGTGA ATGCATTCAT ATATTACTAT ATAAACACTC TCAGCTACAA	200
	TGGTAATATA ATG	213

## 35 (2) INFORMATION FOR SEQ ID :604:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 219 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :604:

5 GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTTCC 50  
TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGA CTGGACC TCTGGTCTCA 100  
ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150  
10 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200  
CTTCAAGAAG AAGAGCTGC 219

## (2) INFORMATION FOR SEQ ID :605:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25

AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50  
CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100  
30 NNGA 104

## (2) INFORMATION FOR SEQ ID :606:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTACCAC 50  
ANNTACAGAA TCTCCACCAT AGCATCAAAA CCAACTCTGA GGAACCTCGC 100  
5 ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA 150  
TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA 189

## (2) INFORMATION FOR SEQ ID :607:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20

GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA 50  
GAGCTCGTAT TTATCCTTTG CTTTNATNTG AGACCAAGCT AGCCCTGAGT 100  
25 AATTTTANNT GGTTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT 150  
GCCTTACGCA CATTCTTTN T 171

## (2) INFORMATION FOR SEQ ID :608:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40

GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA 50



315

TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAAGTGTG 100

ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA 150

5 TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA 184

(2) INFORMATION FOR SEQ ID :609:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :609:

GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC 50

20

CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN 100

TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC 150

25

TCTGTTACAC TAGGTGTAGA GTTCAGAAT GTTCTTTTGT T 191

(2) INFORMATION FOR SEQ ID :610:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :610:

GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT 50

40

GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT 100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT 150

AGGTATGATT TTATAGGNAT AA 172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT 50

T 51

20

(2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTTCA AAAAAATAAA ACAGTATCTC 50

35 TTAATCACTG 60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT 50

CCTGGGCGCA CAGCGAGACT GTCTC 75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA 25

25 (2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

30 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTA CT ATGTTCCGAT CTGTGAATAG CCACTGCACT CTAGCCTGGA 50

TAATATAGTG AGAACCCATC TC 72

40

(2) INFORMATION FOR SEQ ID :616:

318

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10

TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG 50

GGAAATTTAG TGGCAGGGTC CCAAGTGAGCC TGTAAGAAGT GTTCTACTCA 100

15

CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG 137

## (2) INFORMATION FOR SEQ ID :617:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :617:

GCAGGGCAGT CTTGGTGTGC AGCCCCCTCTC CTCTCTGTCC CCTGACACTC 50

30

CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT 100

CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTAC 139

35

## (2) INFORMATION FOR SEQ ID :618:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

319

## (xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5 TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG 50  
TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG 100  
CCTNCNCTGA GGNCNGCCAG GCCATTGTTG ACACCNAC CTCTCNCTG 150  
10 ANNNNCCCAA CCAGCCCCAT TNCCAACA 178

## (2) INFORMATION FOR SEQ ID :619:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :619:

ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50  
25 TTCTGCGGCC GCCACCGCGT GGA 73

## (2) INFORMATION FOR SEQ ID :620:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40 TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA 50  
AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT 100

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

(2) INFORMATION FOR SEQ ID :621:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15 TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCCT 50  
GGAAATGAGC TAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNNCC 100  
CACTTCCTCC CATGCCCTCC AAA 123

20

(2) INFORMATION FOR SEQ ID :622:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :622:

CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA 50  
35 AAAACATTTC NNGAGGAATT TTCAATTTC AGCTTAAAGA ACNNNCCCAC 100  
CAACATAACC AATTATGAA ANNNAATTCA TTAAAAGGTA TAGAACCTCT 150  
TGTNNNCATG ATGGCAAGGG ACA 173

40

(2) INFORMATION FOR SEQ ID :623:

321

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10

TTTATTGTAT CATGAGGCAT TGAACATCT GAATAATCA ATGTCTGGGC 50

GGTGAAGGCA GCTGCTTTCT CCTTCACTTC TTTGGGTAC TAGAGCAACT 100

15

TGTCAGTAGA TT 112

## (2) INFORMATION FOR SEQ ID :624:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :624:

30

ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGGC 50

GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100

AGGTCTGCAT CCCCTCCCC 119

35

## (2) INFORMATION FOR SEQ ID :625:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

322

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20

ATAAAAATCT GAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG

50

35

AAGCGCCACA AGAACATGTC TGACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGCGA GTGCGGCCTC TAGACAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:



323

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :628:

10

AAAAGAAGTA GGTCTGTCTG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG 50

GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA 100

15

CCGGCAGC 108

## (2) INFORMATION FOR SEQ ID :629:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :629:

30

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA 50

CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA 95

## (2) INFORMATION FOR SEQ ID :630:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

CCAGCNCCGA AAAGCCAAGA CTCATCAAC TACATAGGTC TTACCATTGA 50  
5 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100  
AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTG 139

(2) INFORMATION FOR SEQ ID :631:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20

CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC 50  
TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA 100  
25 GCTGAAGTGG TGTGCTT 117

(2) INFORMATION FOR SEQ ID :632:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :632:

CCAGCNCCGA AAAGCCAAGA CTCATGAAC TACATAGGTC TTACCATTGA 50  
40 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100

325

AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTGA GGCCGCCATT 150

GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCAG AATCCAGAAC TTGTCTATC ACTCTCCCA 50

ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC 97

20

(2) INFORMATION FOR SEQ ID :634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTCACC 50

35 TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100

TTCTTCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA 150

GAAGATATGT ATGCAACGTT CATTCAA 178

40

(2) INFORMATION FOR SEQ ID :635:

326

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10

CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC

50

CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA

90

15

## (2) INFORMATION FOR SEQ ID :636:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :636:

CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG

50

GATAAAATGT CATTCAAGAA TGGGGTGAGG TGTTAGAGG GACTAGGTAC

100

30

T

101

## (2) INFORMATION FOR SEQ ID :637:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

327

## (xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT 50  
5 TTTAATAAAG CACAGCACAA 70

## (2) INFORMATION FOR SEQ ID :638:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :638:

CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA 50  
20 ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG 100  
TGGTGTGCTT GGGTCGCTGT CTA CTGCTCC TTCATCAGCT TTGCCAACTC 150  
25 TCGGAGCTCG 160

## (2) INFORMATION FOR SEQ ID :639:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :639:

CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC 50  
40 CGGATCACCT GTTTGAAACC ATCTCCAAG CCATGCTGAA TGCTGTGGGC 100

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

(2) INFORMATION FOR SEQ ID :640:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15 CCGACCACCC CTCCTTTTC TTCGTCCATC CAGCACAGCA AGACCAACGG 50

GATTCTCTTC TGCGGCCGCC ACCGCGTGGA

80

(2) INFORMATION FOR SEQ ID :641:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30

AACTAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA 50

GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA 100

35

(2) INFORMATION FOR SEQ ID :642:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

329

## (xi) SEQUENCE DESCRIPTION: SEQ ID :642:

AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA 50  
5 GTTAATGTTC CATCCATGCT GCTTAAA 77

## (2) INFORMATION FOR SEQ ID :643:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT 50  
ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG 100  
GGCTACAAGG ACTCGCCCTC CGTCTGG 127

25

## (2) INFORMATION FOR SEQ ID :644:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :644:

GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT 50  
40 GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA 100  
AAGTTTATTT TAGACC 116

330

## (2) INFORMATION FOR SEQ ID :645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTGC GGTTTTCAG 50  
GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC 100  
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATACAAG 150  
ACACTCAAGA CAGCAATTAA TCTGTCATCA TT 182

20

## (2) INFORMATION FOR SEQ ID :646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA 50  
ATAAAAATCT GAAAAC 66

35

## (2) INFORMATION FOR SEQ ID :647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40



331

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT 50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT 93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTTG TCCCCACTGA GATGTATGAA GGTTTGGTC TCCCTGGGAG 50

25 TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCA GTTGA 100

AAAGTGCACA CCTT 114

30

(2) INFORMATION FOR SEQ ID :649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

40

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG 50

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50  
AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100  
GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATT 150  
20 AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50  
CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs

333

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :652:

CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTT	50
AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT	100
CTCGAGGACC TGGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA	150
TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG	198

## (2) INFORMATION FOR SEQ ID :653:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :653:

CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG	50
ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG	100
GCATCTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA	150
TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTG	200
TTGCTATAAT AACACTTTTC TTTT	224

## (2) INFORMATION FOR SEQ ID :654:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs

334

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :654:

CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT 50  
10 GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC 100  
CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA 150  
15 AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTGGGTTT 200  
CTGAGCGCAT AAAGCTAAGG AGGGGT 226

(2) INFORMATION FOR SEQ ID :655:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :655:

30

TTAAAAAAT TCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTTC 50  
TTTGGTAACC TGTTTAGAAT TATAAAATC ATTTCATTG GCCCAGCCCA 100  
35 TACGCCCAAG AGAAACTTC CAGACTTTTC TGATGCCATC CAGTTTGTG 150  
CTTACAAAAT GCATATT 167

(2) INFORMATION FOR SEQ ID :656:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

335

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT 50  
TCTGCGGCCG CCACCGCGTG GA 72

(2) INFORMATION FOR SEQ ID :657:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

25 AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA 50  
TACAGAACAA AAAAATTTC CCTTTTAAA ACTAATGTTA CAAATCTGTA 100  
TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAAT AAGGTGTATA 150  
30 GTACAATGTA TTCTAAAACT GTCCGCC 178

(2) INFORMATION FOR SEQ ID :658:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50  
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50  
20 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAACTTC TTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50  
TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT 100  
AAACACTGAT CAACTCAGT TGCCTTACG TTAGCATTAC TCTGTCATAG 150  
40 C 151

337

## (2) INFORMATION FOR SEQ ID :661:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :661:

-----	AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAAGTTCAG CCACGTCTCC	50
15	TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT	100
	CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG	150
	TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC	200
20	TTCACTGTGC CTGCTGAGTC AGCTTGCATC TGCGCCTTCG GTGCG	245

## (2) INFORMATION FOR SEQ ID :662:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :662:

35	GCCAGCGCCG AGGTGCGATA TTTCTAGGCG CAGGTATATG ATTGCCATAT	50
	AATAAAAACM TGAAAACACC CC	72

## (2) INFORMATION FOR SEQ ID :663:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

338

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTGCCTAT CACTCTCCCC 50  
10 AACACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :664:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

25 GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCG 50  
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100  
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150  
30 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200  
CGGATAGTCA CACTCCCTGC CGA 223

35 (2) INFORMATION FOR SEQ ID :665:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



339

## (xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
AATAAAAATC TGAAACACC 70

## (2) INFORMATION FOR SEQ ID :666:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50  
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAAACCACC 100  
TTTCTACGTA CCGTATAG 118

25

## (2) INFORMATION FOR SEQ ID :667:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :667:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50  
40 AACACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

## (2) INFORMATION FOR SEQ ID :668:

340

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50

ACAAGCAGA 59

15

## (2) INFORMATION FOR SEQ ID :669:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :669:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100

30

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

35

CTGCTCCCAG AGCCCACTTT TTT 223

## (2) INFORMATION FOR SEQ ID :670:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

341

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :671:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:

20

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :672:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTGGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

(2) INFORMATION FOR SEQ ID :673:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

342

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :673:

GCCTGCGCCG ANGCAATCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT 50  
10 GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100  
GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC 150  
15 CAAAGTATTA AAAGCAACTT TGCAATT 177

## (2) INFORMATION FOR SEQ ID :674:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :674:

GCCTGCGCCG AGCACAAGAC AATGACGAAC ATTTTAAAAA AAAAGAATGA 50  
CGCACATTTT AATAAAGCAC AGCACAA 77

## (2) INFORMATION FOR SEQ ID :675:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

343

## (xi) SEQUENCE DESCRIPTION: SEQ ID :675:

5 GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG 50  
CCGTAAGTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC 100  
ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACA CCGATTGCAT 150  
AAAATCTTTT TTTAGGAAAA AAACAC 176

10

## (2) INFORMATION FOR SEQ ID :676:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :676:

25 GCCAGCGCCG ACGCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG 50  
CCGTAAGTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT 100  
ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C 141

30

## (2) INFORMATION FOR SEQ ID :677:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 365 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :677:

CTCTGAACAG ACACGAAGCT GCCCCTCGTA CAGCCACTCG GCGGCTGACC 50

344

ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG ACACTGCACG 100  
CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA 150  
5 CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCGC GTGGACCTAG 200  
GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCCCTGGAC 250  
CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT 300  
10 CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA 350  
TCCAGGTGCT GTAGA 365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50  
CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC 100  
30 GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAGGCA GATCTTGACA 150  
GCCTTGCCCG CGAGTGCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG 200  
TGACTGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCCCTGGAC 250  
35 CTGCCGGAGA ACAATACCAC CGCCGCCTNT GCCGCAGTCT TTCCCGGAGG 300  
TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TGCCTGCGGT 350  
40 CATCTAGGTG CTGTAG 366

345

## (2) INFORMATION FOR SEQ ID :679:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :679:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTGACCTAA	100
GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC	150
CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT	200
TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC	250
TTG	253

25

## (2) INFORMATION FOR SEQ ID :680:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :680:

GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG	50
GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC	100
CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT	150

40

346

CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA 200  
AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA 250  
5 GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCTACGG GCTC 294

## (2) INFORMATION FOR SEQ ID :681:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :681:

CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTGACAGCC CCGTGGGGCG 50  
20 GCGGGAGGCC GGGCACTCTA GGTCTACCT ACCAGTGCAA TCGTTTAGCG 100  
CTTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC 150  
25 TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC 200  
TGCCAACCAG AACTGACAGC CGACCTCTG GCGCTGACG CCATTAAAC 250  
CAACGTTGGC GCGCGGCG 268

30

## (2) INFORMATION FOR SEQ ID :682:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 354 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :682:



347

	GCCACCGCCG AGGAAAACCG TGCACTGTTA GCCATGATCA ACCCCACCGT	50
	GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTG	100
5	AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA	150
	AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCTGCT TTCACAGAAT	200
	TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTACACGC CATAATGGCA	250
10	CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC	300
	CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA	350
15	TACA	354

(2) INFORMATION FOR SEQ ID :683:

(i) SEQUENCE CHARACTERISTICS:

- 20                    (A) LENGTH: 148 base pairs  
                      (B) TYPE: nucleic acid  
                      (C) STRANDEDNESS: double  
                      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :683:

30	CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCCT CTCCTCTCTG	50
	TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC	100
	AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT	148

35 (2) INFORMATION FOR SEQ ID :684:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :684:

5	AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA	50
	CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG	100
	CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG	150
10	GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA	200
	TGCTCTTGCC ACACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC	250
	TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT	300
15	GTGAGGC	307

## (2) INFORMATION FOR SEQ ID :685:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 174 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
25	

## (xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30	CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG	50
	AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCACTCTT AGCTGGCAAA	100
	TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA	150
35	GGAGCCATCT CTAGCGGGCC CTC	174

## (2) INFORMATION FOR SEQ ID :686:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 106 base pairs
	(B) TYPE: nucleic acid

349

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA 50  
CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTTACT 100  
TATAAA 106

15

(2) INFORMATION FOR SEQ ID :687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTCCCCCA 50  
GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA 97

30

(2) INFORMATION FOR SEQ ID :688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50  
CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA 100  
5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150  
GAATAGAGTC TAAGCGAACG AC 172

(2) INFORMATION FOR SEQ ID :689:

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20

GCCACCGCCG AGCTCACCCC TCGGGTGCAC GCCTTCCTTG GACAAGTTTT 50  
TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100  
25 TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC 150  
CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC 200

(2) INFORMATION FOR SEQ ID :690:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATCGGGCCCA 50

351

ACACAAATTC ACAAGTGNTC TCAAAAAACT C

81

(2) INFORMATION FOR SEQ ID :691:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15 TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA 50  
TTGAAGGAAG AACCCTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG 100  
TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCCTTCT 150  
20 GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TTCGACTTCA CTCCATAAAC 200  
AGCTGACGCT CAAAAAG 217

25 (2) INFORMATION FOR SEQ ID :692:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTTCCGCACC TCCRAAGGGGA 50  
GAAGACTAAG AGACAGCTTT CA 72

40

(2) INFORMATION FOR SEQ ID :693:

352

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC AGGGGAAGCA 50

GAAAAAGGCA AACAAGAAGA AGGAGGAACC CAAGCAGCTT TCGGCTTCG 100

15

CGTCCAACCC TCTTGCCCTT CACCTACGCG CCTAGAGCCA GTCCCACCAC 150

GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTG 200

CCTTTGACCT AAGCCTACAG CAGGCCCTT TTGTGCTTCC TTCCCCTCAG 250

20

GCAGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTTGTCTTTC 300

CCGATGCTTT TTGTTACCGT GGGGTTTGC 329

25

## (2) INFORMATION FOR SEQ ID :694:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :694:

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGG CCTGCGCCGA 50

ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGCCG CACGGATCCG 100

40

GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG CTGCGGACCA 150

353

GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA 200  
AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG 250  
5 AGCCCACTTT TTTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG 296

## (2) INFORMATION FOR SEQ ID :695:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :695:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG 50  
20 AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGC GCAGAGG 100  
CGTGTCTTAG CACTAACCTC CTCCTAGCC CTTATTTGG TGGCAGAAGT 150  
25 GGCCTCCACC CTTTACCCT TTAATAATAC TCCGTGGAGA AAAGAAAGCT 200  
TNAAGGAGTA G 211

## (2) INFORMATION FOR SEQ ID :696:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :696:

40

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC 50

354

CCAACAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG

92

## (2) INFORMATION FOR SEQ ID :697:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15 GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC 50  
CTACCAGCAA GGGGTCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG 100  
GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC 150  
20 ATAGTCAAGA GAAAGGATT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA 200  
GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT 250  
25 CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC 300  
GCATGCGTAC CTGT 314

## (2) INFORMATION FOR SEQ ID :698:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40 GCCACCGCCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT 50



355

GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT 100  
CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCT 150  
5 CCTTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC 198

(2) INFORMATION FOR SEQ ID :699:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :699:

GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG 50  
20 CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAGTGA ACAGAATGAC 100  
CTTCCTACGC ACAACACAAA CACCAGTTAA TGCTCCATCC ACGCTGCTTA 150  
25 AAGAGCATTG CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCCACCC 200  
TTAGCCGGCA TGCTTACATT AATAGCTAGA 230

(2) INFORMATION FOR SEQ ID :700:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :700:

AGCAACAAAA ATGTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT 50

356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC 100  
AACACAAACA TCACTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCTT 150  
5 GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCCACCCTC ACTTGGCATG 200  
CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA 250  
GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC 282

10

(2) INFORMATION FOR SEQ ID :701:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCAA 50  
25 CATGGATCCG AATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100  
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150  
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC 200  
30 CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAATAAA ATAGCCTGTC 250  
TTTCG 255

35

(2) INFORMATION FOR SEQ ID :702:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

357

## (xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAA AAAAGAATGA 50  
CGCACATTTT AATAAAGCAC AGCACAACT GTTCTTTCC 89

## (2) INFORMATION FOR SEQ ID :703:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCGCTA 50  
GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

## (2) INFORMATION FOR SEQ ID :704:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35 GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA 50  
ACACGGATCC GAATCACCTG GCCCGAAACC ACCTACCTAG CCATGATGAA 100  
40 TGCTGAGGAC CCAGATGCAG TAC 123

## (2) INFORMATION FOR SEQ ID :705:

358

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10 GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCGA GTCCCTCTGG 50  
ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT 100  
15 GCTGAATGCT GCGGACCAGG ATGCACTGCC AGGCATGGGA GCCATTGCCC 150  
ACATCACCGA GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG 200  
GACTAACCCCT GTTCCCAGAG CCCACTTTTT TTCTTTTTC AATAAAAC 250  
20 AGCCTGTCTT TC 262

## (2) INFORMATION FOR SEQ ID :706:

## 25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35 GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG 50  
AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TCGCGAGAGG 100  
CGTGTCTTAG CACTGCCCCC CTCCTAGCC CTTATTG CCGCGGAAGC 150  
40 GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT 200

359

TCAGGGAGT

209

## (2) INFORMATION FOR SEQ ID :707:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15 GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC 50  
TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAGA AGAAGGAGGA 100  
ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTTACCTGT 150  
20 GAGCCTGGAG CCAGTCCCAC 170

## (2) INFORMATION FOR SEQ ID :708:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35 GCCACCGTCG AGGATTACAG AGCCTCCCCC TTGAGCCCCC TCACTTCCCC 50  
ACGTTCCGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT 100  
TCTGCAGGCC GTTCCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA 150  
40 CCCAGAACCT 160

360

## (2) INFORMATION FOR SEQ ID :709:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AACTAAACT GCAAACCTCT 50

15

G 51

## (2) INFORMATION FOR SEQ ID :710:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

30

CAGGATTCTC TTCT 64

## (2) INFORMATION FOR SEQ ID :711:

35

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT 50  
5 CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC 100  
TGGG 104

(2) INFORMATION FOR SEQ ID :712:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20

CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT 50  
TTGTTTTTAG TTGAAGGC 68

25

(2) INFORMATION FOR SEQ ID :713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :713:

AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50  
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100  
40 GTGCTTGGGT CGCTGTCTAC TGCTCCT 127

362

## (2) INFORMATION FOR SEQ ID :714:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC 50  
CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT 90

## (2) INFORMATION FOR SEQ ID :715:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA 50  
ACAAAAATCT GAAAACATC 69

## (2) INFORMATION FOR SEQ ID :716:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40



363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

5 GCCGAGGAGA ACCCCCCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAA 50  
CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATG CAGGCCAGAT 100  
AA 102

(2) INFORMATION FOR SEQ ID :717:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20

AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50  
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100  
GTGCTTGGGA TACGCTGTCT ACAG 124

25

(2) INFORMATION FOR SEQ ID :718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA 50  
TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGCAG 100

40

364

ACAAGGTCCC AAAGACAGCA GAA

123

## (2) INFORMATION FOR SEQ ID :719:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15 ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50  
TTCT 54

## (2) INFORMATION FOR SEQ ID :720:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30

GACCACAGGG CCTTCAATCC TTTTGTGTTT TCAACAGTCT TGCTGAATTA 50  
AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT 100  
35 AATAAACTG TGCACTC 117

## (2) INFORMATION FOR SEQ ID :721:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25

ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA 50

40

TCCCC 55

366

## (2) INFORMATION FOR SEQ ID :724:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :724:

GTGTACTATT AGCCATGGTC AACCCACCG TGTCTTCGA CATTGCCGTC 50  
15 GACGGGCGAG CCCTGGCGC GCGTCCTTG AGCTGTTGC AGACAAGGTC 100  
CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA 150  
TTTGTTATA AGGG 164

20

## (2) INFORMATION FOR SEQ ID :725:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :725:

GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC 50  
35 ACACCCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC 100  
AAGTTCAGTA 110

40

## (2) INFORMATION FOR SEQ ID :726:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs

367

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :726:

CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTTCTTC GACATTGCCG	50
TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG	100
TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
TTTGTTATA AGG	163

## (2) INFORMATION FOR SEQ ID :727:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :727:

GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA	50
GTCAGTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC	100
CTGTT	105

## (2) INFORMATION FOR SEQ ID :728:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

368

## (xi) SEQUENCE DESCRIPTION: SEQ ID :728:

5 GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50  
ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCTT 100  
AGGAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTCGA GGCCGCCACT 150  
10 GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA 186

## (2) INFORMATION FOR SEQ ID :729:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :729:

25 GCCAGCGCCG AGGTTGCATA TTCTAGGCGC AGGTATATGA TTGCCATATA 50  
ATAAAACCT GAAACATCC CACCCGGGAA AAAAAAAAAA AAAAAAAAAA 100  
AAAAACACCC CCCCCCACA AAAAATCAA ATTCCCCTCC CAAAAACCC 150  
30 CCTCAAATC AAAAAAC 167

## (2) INFORMATION FOR SEQ ID :730:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :730:

369

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCT 64

5 (2) INFORMATION FOR SEQ ID :731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCCGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

20

(2) INFORMATION FOR SEQ ID :732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

35 CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA 84

(2) INFORMATION FOR SEQ ID :733:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 96 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA 50

25 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCCACT 50

40 AGCACCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTT TGCCGGG 97



371

## (2) INFORMATION FOR SEQ ID :736:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT 50

15

GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA 100

TACAGCATT ACAAACCGC GCATCTC 127

20

## (2) INFORMATION FOR SEQ ID :737:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :737:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCT 64

35

## (2) INFORMATION FOR SEQ ID :738:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

372

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

5 GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTGCCTAT CACTCTCCCC 50  
AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :739:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG 50  
CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG 95

(2) INFORMATION FOR SEQ ID :740:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35

GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA 50  
GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA 100  
40 CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCGAAGGA 150  
CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT 200

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA

245

(2) INFORMATION FOR SEQ ID :741:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15 GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGCTCTAT CACTCTCCCC 50  
AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :742:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30

GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC 50  
GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA 100  
35 CTCTGATAGT CTTCATTCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG 150  
AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT 200  
CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA 242

40

(2) INFORMATION FOR SEQ ID :743:

374

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

## (2) INFORMATION FOR SEQ ID :744:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :744:

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAAACAT

69

30

## (2) INFORMATION FOR SEQ ID :745:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :745:

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT 50

AATAAAAATC TGAAAACATC CCAC 74

5 (2) INFORMATION FOR SEQ ID :746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC 50

AACACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG 88

20

(2) INFORMATION FOR SEQ ID :747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC 50

35 AACACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT 50  
GCGCTTCCTT CCCCTCAGGC AGCCTCTTC CCCCTGGGCC ACTCCCGGGG 100  
10 GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATCCCGTG GGGCTACCC 150  
CAAAGCATTA AAAGCAGCTT TGCAATTC 178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50  
ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100  
30 AGAAAGGCAT CTTTCGCCAG TGGATTGCC CCAAGGTGA GGCCGCCATT 150  
GGAAGACGAA AAATTGCACT CCCTGGCGC AGACAAACAC CAGTTCCCAT 200  
35 TGGCGCTGCT GCCTATAACA AACACTTTTT TTTT 235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTTC ATCCAGAAAA GCAAGAGAAA 50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT 87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG 50

25 GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC 100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC 150

ATGCCAAAGA CACTCAAAGA 170

30

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50

AATAAAAAAA TGAAAACACC CC 72

## 5 (2) INFORMATION FOR SEQ ID :753:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGCGCCG AGGACACCAA GAAGGTTTTG GACAGCGTGG GCATCGAGGC 50

20 GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAACA 100

TTGAAGACGT TATTGNCCAG GA 122

## (2) INFORMATION FOR SEQ ID :754:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACCGCCG ACTGAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA 50

GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC 100

AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG 150

40

GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG 200



379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

## (2) INFORMATION FOR SEQ ID :755:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50  
AACAAAAACC TGAAAGCATC A 71

## (2) INFORMATION FOR SEQ ID :756:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30 GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG 50  
GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT 100  
35 TAGTGCTTTT TCAGTGGGGC GGGCGGGGAA GCAGGCGGGA CCAGGCAGCC 150  
AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA 200  
GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA 243

40

## (2) INFORMATION FOR SEQ ID :757:

380

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCC 64

15

## (2) INFORMATION FOR SEQ ID :758:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG 50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT 100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC 150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA 200

35

GACGTCGACA ACCAGAACTG ACGTGCAGCC TCCCGGGCGC CGA 243

## (2) INFORMATION FOR SEQ ID :759:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

\_\_\_\_\_

GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG	50
AAGATCACGC TCCCCGCCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT	100
CTTCGCTCTC AGCTCCCCCT GTCCCTCAG CTCCAGACGT AGGGGAGGGG	150
TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTGCTTAAG ATGCTGGTAA	200
TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTT GGGCA	245

(2) INFORMATION FOR SEQ ID :760:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

\_\_\_\_\_

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT	50
AACAAAAACC NTGAAAC	68

(2) INFORMATION FOR SEQ ID :761:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

382

(xi) SEQUENCE DESCRIPTION: SEQ ID :761:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50

5 AATAAAACT GAAAACACCC C 71

(2) INFORMATION FOR SEQ ID :762:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :762:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTGCCTAT CACTCTCCCC 50

20 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :763:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35 GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA 50

GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100

CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150

40 CGCCCATACA GACATCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200

383

CGGATAGTCA CACTCCCTGC CGA

223

## (2) INFORMATION FOR SEQ ID :764:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT

50

AATAAAAATC TGAAACACC

70

## (2) INFORMATION FOR SEQ ID :765:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30

GCCAGCGCCG ACCGCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA

50

TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC

100

35

TTTCTACGTA CCGTATAG

118

## (2) INFORMATION FOR SEQ ID :766:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50

AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50

25 ACAAGCAGAA GCAATAAACC AATCTGATT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

30 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

40

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

5 CTGCTCCCAG AGCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37

20

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35

(2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

386

(xi) SEQUENCE DESCRIPTION: SEQ ID :771:

GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT 50

ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :772:

GCCTGCGCCG ANGCAATCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT 50

GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100

GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC 150

CAAAGTATTA AAAGCAACTT TGCAATT 177

(2) INFORMATION FOR SEQ ID :773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :773:

AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA 50



387

GAATTAGAGG TAAAGGAATC CTAAAATAAA GAGCACAGCA GCAATCACAC 100

TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG 150

5 T 151

## (2) INFORMATION FOR SEQ ID :774:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :774:

ATCTTAATGA ACATGGCATT TAAATCCTG TAATTTCAAA CAGTGAACCA 50

20 CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA 100

CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC 150

25 ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG 200

GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG 250

AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA 299

30

## (2) INFORMATION FOR SEQ ID :775:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG 50  
TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA 100  
5 AACCGTATAT TTAAATGAA TTACTAGAGA GGAATGTAA TCATGGCAAA 150  
AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC 185

## (2) INFORMATION FOR SEQ ID :776:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :776:

20

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA 50  
TTTCACCACA CATGGCAACA AACTTACCTT CTTTAAGAGC GGCAGTAATC 100  
25 ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA 150  
AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT 200  
CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC 250  
30 AACAT 255

## (2) INFORMATION FOR SEQ ID :777:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

389

## (xi) SEQUENCE DESCRIPTION: SEQ ID :777:

	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTCAT AAAGTAAGTT GAA AATTTTCG TTCTTGGCTG AATCGTGTTA	100
	AACCGTTGTA CACAACGTAG TAA AATTCAT AACCCATCTG CATACCAATC	150
	GTCAGCCGTG ATGCATTAC TCACTTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239

## (2) INFORMATION FOR SEQ ID :778:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 252 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25	ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTCCA ACATGCTACA	100
	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG	150
30	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTAAAGG ATGACTCAAC TTCGCCAACT CGGTTCTCTA TTAGGACAAC	250
35	TA	252

## (2) INFORMATION FOR SEQ ID :779:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 265 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

390

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

TCGGATTTAT	ACGGCTGTTA	GTGCTATCGG	CGTCTGGTAT	GTGTTATATA	50
TCGCCTATCG	TTTTTTGGCC	AATGGGCGTT	GGCTACGCGG	GGCAATGATT	100
GCCATCGTTT	TTGTTATCTT	GACTTATTTT	GTCATTTTAA	ATATTATTTA	150
ACTATTTTAC	AAATAAAGTG	GTCAAATGGG	ATATTTTGCC	AAAAATAGAG	200
AAAGTGTTAG	GCGGCCACAC	GCTGGAGGAA	GAGAAAGCGG	CTGTGCATGA	250
AGTTATTGCA	CCCCG				265

## 20 (2) INFORMATION FOR SEQ ID :780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :780:

CTCAGCTGGA	CCAAATTAGT	TGAATTACTC	ACCATCAATA	AACTATAAAT	50
GGCGCCAATG	ACCAACCCGC	CAACGATTCC	CGTTGTCAAA	GAACCTAATA	100
ACAAGTAACC	AACCGCAGCC	CCAACAAGCC	CAACTAGGTT	TAAAAAAACC	150
AAGCAAAAGG	CCAACGTGCC	GTCGTTTATT	GGATTGTATC	TGCTCATATA	200
ACATTAAAAC	TTAACCGTTG	GCACTTCTTT	CTCAGACCCG	CCGATACTG	249

## 40 (2) INFORMATION FOR SEQ ID :781:

391

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :781:

10

GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG 50

CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC 100

15

TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC 150

TTCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA 188

## (2) INFORMATION FOR SEQ ID :782:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :782:

30

AATATTTATT TCATTGTTT ACTACCACTT CATTTTATTT GTTTGCTGCT 50

GCCGTTTTAT TTATTTTAC TGAAAGTGAG AGGGAACCTT TGTGGCCTCC 100

35

AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTGG AACATCTAAC 150

AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT 182

## (2) INFORMATION FOR SEQ ID :783:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

392

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :783:

CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC 50  
CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT 100  
CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT 150  
TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA 200  
CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG 250  
AGAGAATTCA AATGCGTGTT GGTGTTCTCG TTAGTACAAG CAGCA 295

20

(2) INFORMATION FOR SEQ ID :784:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :784:

CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC 50  
GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCACCT TCAGAACCAG 100  
TACCTGATGT TGTGGAATG GCAACCATTT GTGTCAAACG CACTGGTAGA 150  
ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTTGTTT TATTTCCATG 200  
AACAAATTCCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT 250

40

393

TGAGTATTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

## (2) INFORMATION FOR SEQ ID :785:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :785:

15 GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA 50  
CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTGGGTTTTTC 100  
ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC 150  
20 CGAGGCTGCG CAGGAGGTGA CGTCAAGATG TGGCCAATAA AGTCCAAAAA 200  
GCGCTTTGAA TACTGTTCTG GGTTCACGGT GGAGATCTCC GCGCAGCCAT 250  
25 GTTTAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA 300  
GTA 303

## (2) INFORMATION FOR SEQ ID :786:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :786:

TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT

50

394

CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT 100  
ACATGAAGAA TGATGGTGTG CGTGGGGCCA TTAAGTACTA AGCCAAGAAG 150  
5 TTATCACGAC AACCTATAAC TTGGGCCGAA TTAAGTTGAT GATGCACGGG 200  
GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA 250  
CTGGC 255

10

(2) INFORMATION FOR SEQ ID :787:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :787:

CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG 50  
25 TCAGAATCAA CAAACTAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG 100  
GGCATGATAC AAACCACTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG 150  
ACTTATTTTT ATTTTTTTTT TTTGGACAG ACTCCCTTGG TCCCCAGGCC 200  
30 GGAGTG 206

(2) INFORMATION FOR SEQ ID :788:

35

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



395

## (xi) SEQUENCE DESCRIPTION: SEQ ID :788:

ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT 50  
5 CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG 100  
TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTTCAAAC GAGGCGTGGA 150  
AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG 200  
10 GAACAATTCC GCGACACCCT TCGTCTGACA AAAACCTTC GTGACGCGTC 250  
GAGTATCCGC 260

## 15 (2) INFORMATION FOR SEQ ID :789:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC 50  
TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT 100  
30 GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCCGCACT 150  
TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG 200  
35 ATCGACGC 208

## (2) INFORMATION FOR SEQ ID :790:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

396

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

AAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT 50  
GAAAATACAT TGTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC 100  
10 ACTCTTGCTA TCGACCATCG TCGCGCTTGG GATGAACCGT CGTAAGTCAC 150  
AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT 200  
15 TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG 250  
TCGTTATCCA TGGGTGTTT ATGGCTTGAT GCTAATAGC 289

## 20 (2) INFORMATION FOR SEQ ID :791:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :791:

TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAAATT TGGCAATTAA 50  
TTGCTCATT TTAATGGTAG AGTTTCATT AATGAAGTTG GAAAATACGG 100  
35 TGAATCTTTC AATGAACTCA GTTAGACATT CGGAATGAGC TTCATACATT 150  
GTCTTATTAT CTTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAA 200  
CCAAATTGAA GCACCTTATC TATGATCCGG GC 232

40

## (2) INFORMATION FOR SEQ ID :792:

397

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC 50  
TGGTAATATC GAACAAACTA TTTTAAAGAA CTGATTCTTCT GGCAACATTA 100  
AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG 150  
GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA 200  
TGCCTATTTC GCGAAGTATG GATCTAAATA AC 232

20

## (2) INFORMATION FOR SEQ ID :793:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTACGGTA GTGANCCAG TGACCAGATG TCTTATACAA 50  
GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA 100  
ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC 150  
ATTTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA 200  
ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTACAGTTC TTAGCTTCT 250

40

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT

292

## (2) INFORMATION FOR SEQ ID :794:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 288 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15 CAGCAGGCAC AACACCATCG GTTGTGCTG AAAGTATTTT TAAGTCTTTG 50  
GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACCTATG CGGGTATGCA 100  
TGATGTCATT CCTGCATCCG ATGATTTTTA ATTAATTACA ACAACTGATG 150  
20 ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA 200  
GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC 250  
25 CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC 288

## (2) INFORMATION FOR SEQ ID :795:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :795:

GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT 50  
40 CGATAGACCC AAAAAGTGTT TTAAGTGGAA AACACCTTAT GAGGTTTATT 100

399

TTGATGAAGT GTTGCAAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT 150  
CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTC 200  
5 GAGGTCAGTT ACGGCGTCCA GTCTTTGAGC AGATGATTG CCCCAGTGA 250  
TCGTCGGC 258

## (2) INFORMATION FOR SEQ ID :796:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :796:

20

TGCTTCAAAG CCTGGCTTAA CCCGCTGCC CACCACTTC AATTATACCT 50  
GCCCCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC 100  
25 CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACA TTTAACACAC 150  
AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG 200  
AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG 250  
30 CTCATGTAAC GCGACAATAT 270

## (2) INFORMATION FOR SEQ ID :797:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

400

## (xi) SEQUENCE DESCRIPTION: SEQ ID :797:

	AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC	50
5	TTGTGTAGGT TGTCTGAAAC GGTGCGAGTC ACCGGTTAGC TTGATAAGTC	100
	AGGTTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC	150
10	AATCGCACTT TACATCATTAG ACCCTTAC TAGAAGTAAC TGGCCATCCT	200
	GCCACCGCTT	210

## (2) INFORMATION FOR SEQ ID :798:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :798:

25	ATCATAAGCG CTGGAAGTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT	50
	GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA	100
	CCACGGTCCA AGGCAAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA	150
30	TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCCAAA TAACGAGACA	200
	AGTAGTTGAG CTAAATGC	218

## 35 (2) INFORMATION FOR SEQ ID :799:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 176 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

401

## (xi) SEQUENCE DESCRIPTION: SEQ ID :799:

5	CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG	50
	AGAATAGCAT TACCAAATGG AACAACTGC TACAGTCAGG ATTAAAAAGA	100
	ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG	150
10	AACAATACAA CACTGAATTA CTCGGC	176

## (2) INFORMATION FOR SEQ ID :800:

## (i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :800:

25	GCAATTGCTT AATTGTCT TCCTCTTAG CATTTTGCTG AGAAGCCAAA	50
	CGTTGCGCCA ATTCAGAAGA TTCAGCCAG AAGTCGTAGT TACCAACGAA	100
	TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT	150
30	TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA	200
	GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT	250
35	TCGA	254

## (2) INFORMATION FOR SEQ ID :801:

## (i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 203 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

402

## (xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5 ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA 50  
TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT 100  
AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT 150  
10 AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA 200  
ATG 203

## 15 (2) INFORMATION FOR SEQ ID :802:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

GACACAAGTG TGTTCCTAG CAACCTCAAA CAGACACCAT GGTGCACCTG 50  
ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG 100  
30 GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG 150  
GACCCAGAGG TTCTTTGAGT CCTTTGAGGA TCTGTCAACT TCC 193

## 35 (2) INFORMATION FOR SEQ ID :803:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



403

## (xi) SEQUENCE DESCRIPTION: SEQ ID :803:

5 AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA 50  
AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC 100  
AATAGCGTAC AGATTTTTC GCATTAATCC GTGTTTATAT TAACAGATTC 150  
10 GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCCTCT CTCTAGATAA 200  
ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTCTAAA 250  
CGATAACAAG AACCCAGTA GGTAGTATAG CAGTCTTTAA 290

15

## (2) INFORMATION FOR SEQ ID :804:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :804:

AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA 50  
30 AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC 100  
AACATTTCCG GCAATTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT 150  
CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCTAC CACTTCCGGG 200  
35 CCCCCAGCCG CATATCCGG CGGACCGTGC GAGGTATGCT GTCCACAAA 250  
ACAGGG 256

40

## (2) INFORMATION FOR SEQ ID :805:

## (i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10	AGCAACCTCA AACAGACACC ATGGCGCACC TGA	50
	CTCTGA GGAGAAGTCT	
	GGCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA	100
	GTCGGCGGGC	
	AGGCCCTGGG CAGGCTGCTG ACCGATTAC CTTGGACCC	150
15	AGAGATTCTT	
	TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG	200
	GGCAACCCTA	
	AGACGAAGGC TCATGGCAAG AAAGTGTTGC GTGCCTTTAG	250
	TGATGACCTG	
20	GCTCACCTGG ACGACCTCAA GGCACCTTT GCACAC	286

## (2) INFORMATION FOR SEQ ID :806:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :806:

35	TTCTTCATCA GATTTTACAT CTGCCTGATT AGAATCTTCT	50
	ACACTGGCCT	
	CAGAAGATGA TTGTTCAAAA CTTTTTCTAA GTTGCTGTAA	100
	AAAAACTTCC	
	ACGGACAAAG TAAAATGCAG TTCTTTATCG TTTAGCCAGT	150
	GTACAACAAA	
40	AGGTCCAATC TTCTCTTCAT TTTAATTCAG ACTCAGAGAT	200
	GTAATAGATG	
	GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC	250
	AATATGAAAG	

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

## (2) INFORMATION FOR SEQ ID :807:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :807:

15	AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTATTAG GCAGAATCCA	50
	GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG	100
	GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAGAAAG CGAACTTAGC	150
20	GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG	200
	GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC	250
25	ACAGACCAGC ACGTCGCCCCA GGAGCC	276

## (2) INFORMATION FOR SEQ ID :808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :808:

40	GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT	50
	CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA	100

406

ACATCGCTAG CTAATTTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG 150

AAGCTTGTTTTC TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG 200

5 ACGTGATCGC TTATCGTA 218

## (2) INFORMATION FOR SEQ ID :809:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 276 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :809:

AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA 50

20 CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT 100

TACTGCCCTG TGGGCAAAGG CGAACCGGGA TGAAGTCGGC GGCGAGGCCC 150

25 TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC 200

TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCGAAG 250

ACTAATGGCA AGCAAGTGCT AGACGC 276

30

## (2) INFORMATION FOR SEQ ID :810:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC 50  
CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTCCTTCT 100  
5 GAGGAGGCTT ACTGCTTTTC TTA CTGATT TATTTTCAG AGTTTCTTC 150  
TTCGTACTTT TTTAACGCA AGTATTTTGC TTTTATTCT CCTCCATT 199

## (2) INFORMATION FOR SEQ ID :811:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :811:

20

AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA 50  
AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC 100  
25 TGGGGGGCTT GCGGTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA 150  
GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT 200  
TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT 250  
30 AAGT 254

## (2) INFORMATION FOR SEQ ID :812:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

408

## (xi) SEQUENCE DESCRIPTION: SEQ ID :812:

TTTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA 50  
5 CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA 100  
CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA 150  
CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCTTC CAAACAGGCA 200  
10 ACCTGCACCG GAGGGGAGAC TTTTCGCCA AAGCGACGGG CCAGCACACA 250  
GACCAACACA TCGCCAGGA ACCTGAAGTT TTCA 284

## (2) INFORMATION FOR SEQ ID :813:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

ATACAACAGC AGAAACAGGT ATCCACGCAC AGTCCAGCAA CATTCTTCT 50  
GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA 100  
30 GGCAAGGATG CTAACGCGAA GTCAATCAGC CGAGTGATGT CATTACAAC 150  
CGGTACCGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG 200  
35 CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAG AGCTAGACGA 250  
CTGACGAAAC CTGAGAACCC CGAAGGACT 279

## (2) INFORMATION FOR SEQ ID :814:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs

409

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :814:

10 AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC 50  
ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA 100  
CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG 150  
15 GCGGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC 200  
AGCAGCCA 208

## (2) INFORMATION FOR SEQ ID :815:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :815:

30

AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG 50  
CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG 100  
35 TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC 150  
AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA 192

## (2) INFORMATION FOR SEQ ID :816:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs

410

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :816:

GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG 50  
10 CCGCCTGGGG TAAGGTAGGC GCGCACAATG GCGAGTATGG TCGCAGAGGC 100  
CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA 150  
15 CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG 200  
GTGCCCAGCG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCAAC 250  
GCGCTGTCCC CCTG 264

20

## (2) INFORMATION FOR SEQ ID :817:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :817:

ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA 50  
35 AAAACCACTC AACAAGCAAA CAACCCATCC TGTTTTTATA ACGTTATCGT 100  
AAC AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA 150  
AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA 200  
40 TG 202



411

## (2) INFORMATION FOR SEQ ID :818:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA 50  
TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA 100  
CTGTATAGTT TTTTAAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC 150  
CCCATAGGAT AGGTAATGAA CTTTTTGT 179

20

## (2) INFORMATION FOR SEQ ID :819:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAACT 50  
AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAA AAGAATTTAA 100  
GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT 150  
CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAAGTG GATCAAGTTG 200  
TACGCGGGTC CACGAAGTGA CAGACGAAA ATGAACGCAA GCTGATGTAA 250

40

412

ACGCATCACA

260

(2) INFORMATION FOR SEQ ID :820:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 226 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15 ACTCGGCACT TTCTTAGAAT AGACAATTG CAAAATGTCC ATCCCAGGTT 50  
CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG 100  
TGAAC TT TAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC 150  
20 ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC 200  
TTTCCGTAAC TGAGTTTGAT TTCTCC 226

25 (2) INFORMATION FOR SEQ ID :821:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTTT TGGTTGTAA 50  
TTTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA 100  
40 GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC 150

413

GTGATTTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC

197

## (2) INFORMATION FOR SEQ ID :822:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15 GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG 50  
GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG 100  
GCAATCTCAA TGGCACCGCA AGCTAAATGA CTCCAGTGT TTCTCATCTT 150  
20 TGCGCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT 200  
CACCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT 250  
AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA 300  
CATG 304

## (2) INFORMATION FOR SEQ ID :823:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :823:

40

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG

50

414

GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG 100

CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG 150

5 GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG 197

## (2) INFORMATION FOR SEQ ID :824:

## 10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20 AAAACAATG TCATTTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA 50

CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT 100

GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCCTGACT TACCCTGGCA 150

25

GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTCCTTA ATAGCAATGA 200

TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCCAG ACAGCAAGCG 250

30 TTTTCCACA GGTCTCGACA CACAGAAGAT A 281

## (2) INFORMATION FOR SEQ ID :825:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 312 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

TATTAAATTT ACTAGAATGT TACAGTTACA AATTGGTAA TGTCTTTCT 50  
GAAAAACAGC CTAATTTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC 100  
5 TTTTATTCAT GATAGAAAAA TAATTCCTGG CTCATCTCA CAATTAATA 150  
ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTTT TCAGTGATGA 200  
TCAAAGTGAT TCTCCCAGGC CAAAAATCA AATAAGAAGT TATATTTTAA 250  
10 AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT 300  
CTACTAATTG GC 312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA 50  
GGGCAGGGAG GGGGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA 100  
30 TCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCCC CCGGGTCTCA 150  
GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA 189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

416

## (xi) SEQUENCE DESCRIPTION: SEQ ID :827:

5 CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT 50  
ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA 100  
AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT 150  
10 TTAGAGATTA TTTTGTGGCC TGGAAATCTG TCTCATCACA GAGTGTTAAT 200  
ATACACCGGC GGGATATTCA AGAGTGGCTA AG 232

## (2) INFORMATION FOR SEQ ID :828:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25

GGACATTGGA ACACTATACT CTATTATTGC GGTCGTCCT AGCAGTCTCG 50  
CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT 100  
30 TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC 150  
TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT 200  
CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA 250  
35 GTAATTACCC CATATCATAA AATGCGGGCG GG 282

## (2) INFORMATION FOR SEQ ID :829:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid

417

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

	CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC	50
10	TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA	100
	AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCGCTTC AACGTGCTCA	150
	AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCCAGAA GTTCTGAGGC	200
15	TGGACATCGG CCCGCTCCCC ACAATGAAAT	230

(2) INFORMATION FOR SEQ ID :830:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 226 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30	TTCCGCRAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA	50
	GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAAATG	100
	GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA	150
35	TAAACTTAAC AAGAAATGTT GCAAAACCAT TATGTGAAAA TTACAACACT	200
	CCTGAAGACG CAGACACACC TAACAA	226

40

(2) INFORMATION FOR SEQ ID :831:

- (i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10	AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTTCCTT CTTTCTACA GCCTGCAGTT CATTTAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT	200
	GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT	247

## 20 (2) INFORMATION FOR SEQ ID :832:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

	CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112

## (2) INFORMATION FOR SEQ ID :833:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid



419

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA 50  
10 ATGTTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAAGTA AACTCAGATG 100  
CCTGAGTGCT TGTGGCCACC ACACAACAGA TCGGGCCTTC CTCTTCACTG 150  
GCCCCTCGGC TGCTGCTGGG TCC 173

15

(2) INFORMATION FOR SEQ ID :834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs  
20 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCCTT ATGACACAAT 50  
30 TCCATCATTC TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTTC 100  
CAGACTTATC TTATATTTTC ACTTCCCAT ACCTGGAATC AATCACTTCT 150  
CCGAGGATGC TTGATTCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC 200  
35 GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG 250  
AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT 288

40

(2) INFORMATION FOR SEQ ID :835:

(i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :835:

10	CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAACCAG CAAGTTTTTA	150
15	TTAGTGATTT TAAAAGGGGA GGGAGTGAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTTACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	310

## (2) INFORMATION FOR SEQ ID :836:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :836:

35

	TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTTA	150
	CATCTCCCAA AATGCCTAGC ATTCTTC	177

421

## (2) INFORMATION FOR SEQ ID :837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC 50

15

CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA 100

TGTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT 135

## (2) INFORMATION FOR SEQ ID :838:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :838:

30

TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT 50

GAAATGCCAA GGTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA 100

35

GAGGTAATCA AAAACTCGAG CATGTATTTC AGGATCCATG ATTGAATTTA 150

CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA 200

G 201

40

## (2) INFORMATION FOR SEQ ID :839:

422

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10

TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA 50

GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA 100

15

TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT 150

CTGAGATGTA CACGAACGAG ATCTTTTGAG A 181

## (2) INFORMATION FOR SEQ ID :840:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30

CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG 50

TTTtagTGAA CATTcAGAGG AGTTTGAAG AAAGTCGCTG CACAATCTTC 100

35

ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA 150

TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA 200

TAATAACATG GGTTTAAAAA AC 222

40

## (2) INFORMATION FOR SEQ ID :841:

423

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10

CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCTTGCT CTTGCTGCGG 50

CTCCTATCTA CCGGCTACCT GCTGCCCCTG TTGCTCCTGC TACCGGCTCC 100

15

GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCTGCT CACAACTCCC 150

TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC 200

TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT 250

20

GTCATTGTTT TGGAACTTCT CCTTCAGCTT GGTCTTTTGC CGG 293

## (2) INFORMATION FOR SEQ ID :842:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35

ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC 50

TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTTT TGGCAGGTCA 100

GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCCAA GACACACAGG 150

40

AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC 200

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAAAA

239

## (2) INFORMATION FOR SEQ ID :843:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15 TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTTC 50  
AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA 100  
CTCACTCACT CTATAATAAA ATGTTTGCAC TCAATTTATA TAGTAGTGTT 150  
20 TGTC 154

## (2) INFORMATION FOR SEQ ID :844:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 392 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35 GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG 50  
CCAGGACTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC 100  
TACTCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC 150  
40 TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCCTCAGC CTACCCTATC 200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCCTAG CAGGTTCCCC 250  
ATCTTTTCCA GGCTGCCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG 300  
5 ACAGGCCCTT TTTGGGTACC TAAACCCAG CTGAGGTTGT GAGCTGTAAG 350  
GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT 392

(2) INFORMATION FOR SEQ ID :845:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20

CAAAGAATAA ATAATTTTTC TATTCCTGAA AGTAACTAA TTATTTATTA 50  
GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTGAGA AAGTGATATG 100  
25 AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT 150  
GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA 200

(2) INFORMATION FOR SEQ ID :846:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40

TTAAAAATAC TCTGGAAAGA GCACTTCCAT CGTTCATTTA CATCATATTA 50

426

5 GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG 100  
AGGAGCGAGA TCTCCCAAG CCTCCAGGAT TGCAGTCTGT TTGTGCCTT 150  
CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC 200  
AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC 250  
ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA 300  
10 GAGGAGGTGG T 311

(2) INFORMATION FOR SEQ-ID--847:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

25 CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA 50  
CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC 100  
GGCAGGA ACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC 150  
30 CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG 200  
GCAGCTCGAG GCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG 250  
35 CCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT 287

(2) INFORMATION FOR SEQ ID :848:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



427

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC 50  
TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA 100  
10 TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG 150  
AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AACTATACA 200  
15 AACACGCAAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG 250  
AGGCATATNA CCA 263

## 20 (2) INFORMATION FOR SEQ ID :849:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :849:

TTGTCAGTCA GAATAGGATG TAAAAGACTA TTTCAAAGAG TTAAATTATT 50  
TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG 100  
35 CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT 150  
TGACATTAAA AACGAATGGA TACCCAACCTC TGAATTCCAT ATCGTTTTTTT 200  
AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA 250  
40 GTTTATCGAA ATCCTGCCGC TACTAAACA 279

428

## (2) INFORMATION FOR SEQ ID :850:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC 50  
AGCATCTGGA TAAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT 100  
GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA 150  
TGTTTATGAG CTCTCGACAG AAT 173

20

## (2) INFORMATION FOR SEQ ID :851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA 50  
TGGAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG 100  
TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG 150  
GGACTACAGC AACAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC 200  
AGCAGGAATT TTCTGTAA AATATTTTTG CCGTAATACT 240

40

429

## (2) INFORMATION FOR SEQ ID :852:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :852:

ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGGAAATGTTA 50  
15 AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACAAACATCT 100  
GCTTATTATG AAAGTGTTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC 150  
CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA 200  
20 TTCCTCTTAT AAAACAAGGG CAATTTTGTG AGAGCTACTG ACGATTTTCC 250  
CCTCGAAATT TACTATTCTT ACAGCTTATT AATCTCAAAT AGTAAGCATG 300  
25 TCCTTGCCGT CACT 314

## (2) INFORMATION FOR SEQ ID :853:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :853:

TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA 50  
40 CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTGGT 100

430

ATTCTTCAG TGACAAGCAA ACTATCCCC CACATGCCTT TAATGGCCAG 150  
TGTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA 200  
5 CTGATACGCT AACCTTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC 250  
GCGCCAATAC TGCTTAA 267

(2) INFORMATION FOR SEQ ID :854:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC TTTCTTTTTT TCCAAAGGAA ATTCATATA GAGTCCATTC 50  
ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG 100  
25 GCTTGGAGCC CCCAGCCTCT TTGCTTTCTC TTATCCCTAT AGGATGGCCA 150  
TTAGGTGAAG CAGTTTAGCT TGTGGTTCA GACCTG 186

(2) INFORMATION FOR SEQ ID :855:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATTT CATAGTCAGC 50

431

CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG 100

GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT 150

5 GGCCCAAAAA TT 162

(2) INFORMATION FOR SEQ ID :856:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :856:

TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA 50

20 GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT 100

GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG 150

25 GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC 200

AACATAACAA ACCCAATCGC CCTGTAACT TTAAATCTTC AACTCGAGAA 250

AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC 286

30

(2) INFORMATION FOR SEQ ID :857:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

AACTATATGG TATTATTTC ACGCTGTACCC AGTCCATTGC TTGAACTTAC 50  
GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTTT 100  
5 CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG 150  
ATTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC 200  
TTTTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTTCT GTTACTTAAT 250  
10 CGGCGCCAAG GCCTTTACAT GAATACTCAG 280

## (2) INFORMATION FOR SEQ ID :858:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25 CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG 50  
GCCAGGCTGG TCTTGAATC CCAGCCAACC TCAAAGTGCT GGGATTACAG 100  
CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAAA AACACAAGTC 150  
30 CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTTACAT 200  
CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT 250  
35 TATACAGGGC TTGAACTGTC TTTAAGCAA GCCCCAAATC CTTTGAAAGG 300  
AGGCAGTAAC 310

## (2) INFORMATION FOR SEQ ID :859:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs

433

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

10	TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG	50
	CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT	100
	CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC	150
15	AGGAAGAG	158

(2) INFORMATION FOR SEQ ID :860:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

30	TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT	50
	CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA	100
	TTACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC	150
35	AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT	200
	TAGATTCGGA ATAACCTGAA AATAAATCCC AACCACGTAA CTTACTAAAG	250
40	GAATAATGAG CCA	263

(2) INFORMATION FOR SEQ ID :861:

434

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10

ATTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG 50  
GGCATTCTAT TCCTAAGAAT GTCCTAAAA TGGAAACTG ATAAAAGATT 100  
ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGTTT 150  
TGATCCCATG GGTCAATTGT TATTACTCTT CTTCAACAGA GTGATTTTCT 200  
ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG 250  
AAAG 254

20

## (2) INFORMATION FOR SEQ ID :862:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35

GTCCTCCTT TGTAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT 50  
GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC 100  
CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGCTGTC 150  
TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA 200

40



435

TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC 250

TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT 300

5 TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC 337

(2) INFORMATION FOR SEQ ID :863:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :863:

TGGTGGGTTC GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC 50

20 GGTGCGGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC 100

TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA 150

25 ACTTACAATG CCACCGCGA 169

(2) INFORMATION FOR SEQ ID :864:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :864:

ATTAAGGTAA AGGAAGACTT TCCATTGTGA AGTAGAAAGA GTGTCCTGCT 50

40 ATTACTACCA TTCACATCTA GTTGTGTGA ACTAGGGTTT TCTATCTTAA 100

436

CCCTGTAAA AACAAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG 150  
CGGATAGCAT TATCTTCCTG TGTTCAGAC TGAATGAAT TTATGAACAA 200  
5 GGCAAGCACA CCATTATAGT AAATAAAATC TTACCTAGT TTCGTTTTTG 250  
CATTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC 286

(2) INFORMATION FOR SEQ ID :865:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20 ATATAGTCCG CTAGGGATAG TGAAAAATTT GGGGCTTGGT TTAGATTGGA 50  
GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG 100  
25 GCCTTGATTT CTGTCCCCCT TGCCTTGCGT GGCCTTTGAA TTGAAAGCTT 150  
TGAATTAGGC CTCATAGAT TTAGTGTGC ATACAAATAA CACGATCTTT 200  
TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC 250  
30 GCATTCTGA TCTATAAGGT GA 272

(2) INFORMATION FOR SEQ ID :866:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

437

## (xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAACTAAGT CAAAAAACG GAACGCAAT 50  
5 AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG 100  
GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG 150  
CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG 200  
10 TTTCTAACAC TACAACGCTA ACTTTTGGAA CGTATCTACT TCTAGCATGT 250  
AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG 296

## 15 (2) INFORMATION FOR SEQ ID :867:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG 50  
CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA 100  
30 CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT 150  
CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT 200  
35 GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A 241

## (2) INFORMATION FOR SEQ ID :868:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC 50  
ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT 100  
CAAAGCCCAA TATAACCAAG GGAAGGAAT 130

## (2) INFORMATION FOR SEQ ID :869:

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :869:

25 TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTGAAAAA 50  
CTAATGAGAA TGCCATAAAC AACATTAAAG CAATATATTT TGAAATTTAA 100  
TTCAAATGGT CAAATTCCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT 150  
30 TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA 200  
TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT 250  
35 TCCCAAGCAC TTAACAATA AACAATGCCC TCTTTATACA AACCTTTCCC 300  
AGTAATAGAA 310

## (2) INFORMATION FOR SEQ ID :870:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs

439

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :870:

AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTAGGCA	50
TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC	100
CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG	150
CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG	192

## (2) INFORMATION FOR SEQ ID :871:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :871:

ACCATAGATG TGTTCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG	50
AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCAGAT CTTTCTACAT	100
TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA	150
CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTCATGGAG ATTTGAATAA	200
TCTATCCGAT GAGATTTATA TNTAAACAAC TCAACTCCTG TCGAAACAAA	250

## (2) INFORMATION FOR SEQ ID :872:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs

440

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :872:

10	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
	AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG AACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
	TTCGTGGCCA GGGAAACACA TGTTCOAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313

## (2) INFORMATION FOR SEQ ID :873:

- |    |                               |
|----|-------------------------------|
| 25 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 270 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC	100
	ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT	200

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAACT 250

ATCCAGCGTT AGCACAAATG 270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTT ATCTCCAAAG CCAGCCATGG TGTATTTCTC 50

TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT 100

20

GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT 150

TAATGACAGC TGATTATTTT CATCTGCAAA CTTACTCAAG AATGCAATCC 200

25

AGACTAACAC GACAATAGGA CATCAAGCT 229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAAC TTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC 50

40

CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT 100

442

TGGTCTTGAC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG 150  
AAGGCTTTTG TGTTCCTCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA 200  
5 AGCACCGTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT 250  
ACACGGAACG GTCCTCGACC CGTGGGTAAC AGTATTTTCT GCGT 294

## (2) INFORMATION FOR SEQ ID :876:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :876:

20

ATTTTGGTA ACATACATCA AGTGGCACTA ATTACACACT AACTATAAGG 50  
TAACTAACAT GAAACCACAG AACTGTAACT CTGCCACAGC TGCATGAACT 100  
25 CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT 150  
ACGCCAACAA AAACCGTTAT TAA 173

## (2) INFORMATION FOR SEQ ID :877:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :877:

40

TAATCAAAAG AGCTCTAAAT CTGTAATTTC TTTCTCCTTT AAAAAAATGT 50



443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG 100

AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTTCG AAC 143

5 (2) INFORMATION FOR SEQ ID :878:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTCAG TGGTTCCTGC TGTGGGACTT 50

GCGTTTTCAC TAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC 100

20 AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA 150

GGGCTTCTAT TGCTAATGCC TGTAACCTT GCTGAATCTA TAACAGAGTC 200

25 TATACCGCTC TCG 213

(2) INFORMATION FOR SEQ ID :879:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA 50

40 ACGAGATAGA CACATGCTTA TTCAAACCAC AGATATGATC CAGTTAATTC 100

-444

CCTTCTTAGA ATGTGCCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT 150  
AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC 200  
5 TACCAGAGTA ACCGTCATCC CCTTGAG 227

## (2) INFORMATION FOR SEQ ID :880:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :880:

ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG 50  
20 AAGCCTCAGG AATTCCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT 100  
TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA 150  
25 TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA 200  
ATAATCACTC TTTACAAGGT A 221

## (2) INFORMATION FOR SEQ ID :881:

30

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :881:

40

AATTGTGGTA TATTTCAATTT AAAATCGATC AAAGACAGCA ACATACATTA 50

445

	ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT	100
	CATATTAAAA CAATGATAAG TAATACTTAG AAAGTGCATC CTAGAGACAC	150
5	ATCATTCGCA TTTTGTAGAA AACAGAAACA TATTAGTGTG AAAAGATGTT	200
	AAAAAATGAA TATTAAACCG TCGAGCACAA CACACTACGC CGATAACAAT	250
	ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT	300
10	GGCGATCCGA	310

## (2) INFORMATION FOR SEQ ID :882:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 177 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25	GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT	50
	GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA	100
	CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA	150
30	CGAACTACAA ACGTAACAGC AGCAGGC	177

## (2) INFORMATION FOR SEQ ID :883:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 152 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCTCTGA AGATACACGT 50  
5 ATAAACGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100  
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150  
GA 152

10

(2) INFORMATION FOR SEQ ID :884:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50  
25 GACCTATTTT AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT 100  
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150  
AAATGAAATT GTGCCGAAAT GTATACA 177

30

(2) INFORMATION FOR SEQ ID :885:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAT 50  
TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAAGTAGAA 100  
5 TTTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT 150  
GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTA CAAATATATA 200  
TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A 241

10

(2) INFORMATION FOR SEQ ID :886:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

GTAGCAACCG GCGCTCAATA AAATCAACC AGCAAACTCG ACAAGTAACA 50  
25 ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA 100  
ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG 150  
CCATCCATAT ACCAAAAATG CTAATTACAA CACCACAACA 190

30

(2) INFORMATION FOR SEQ ID :887:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA 50  
CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA 100  
5 CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA 150  
CTATAATATT ATACTCTC 168

## (2) INFORMATION FOR SEQ ID :888:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20

ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT 50  
GCCGATCTCG CAACCGGTTT CAGTTAGACA GAACATTGTG ATATTCAAAC 100  
25 CACTTTCTCG TAATTTCCTA TGGAGTTGTA AAGTTTAATG AGACCTCGAT 150  
AATCATATTC TAGTCCACTG TAGC 174

## (2) INFORMATION FOR SEQ ID :889:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40

ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA 50

449

TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA 100  
TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT 150  
5 ATATGTGTGT GTACAATATA TAAAAAATTA TATGGGAGAA AAGAAAGGCA 200  
AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTTG TGTGTAACAA 250  
AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT 300  
10 ATATATATAT CTGTATATAC AGGTATA 327

## (2) INFORMATION FOR SEQ ID :890:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25 TTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC 50  
GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC 100  
TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT 150  
30 ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T 181

## (2) INFORMATION FOR SEQ ID :891:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

450

## (xi) SEQUENCE DESCRIPTION: SEQ ID :891:

CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCTCAC 50  
5 TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT 100  
TTACTGTT TGAAGCATCT AACGAAGGC AACAGTTTTT GGCAACCCAA 150  
TTCACAGTTT TGTAATTTAC AAGAGATTC TTTGAAAGGA AATAGGAAGG 200  
10 CAAAGAA 207

## (2) INFORMATION FOR SEQ ID :892:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :892:

25 CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG 50  
TGATTTTACA GTAGAGTGAA CGAACTTGG GAAGGAAAC ATCCAAGAGG 100  
CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT 150  
30 TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAACACTC TCTACTCT 198

## (2) INFORMATION FOR SEQ ID :893:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40



451

## (xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT 50  
5 TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG 96

## (2) INFORMATION FOR SEQ ID :894:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :894:

AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA 50  
20 ATGGAAACAG CATAATACTA CATACTATCG CGCGGGGTTG TCGGCGTGGT 100  
GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA 150  
25 GAGTGAGCGT GGGAGGGTGT GGTGCGTGGA GGTGTGTGGA GAGGTGAGTG 200  
TGCGAGAGGG GCGAGTGTAT GTGTGATAAG TATAGCGCGC AAGAGGCGAG 250  
GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAAC 300  
30 AATAACCACT ACTCACATAG AATAT 325

## (2) INFORMATION FOR SEQ ID :895:

## 35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

5      ATAGTTGTAC ATTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC      50  
AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA      100  
TTTATCATTT ATTTGTGTG GAAACATTCA AACCTTTTCT TCTAGCTATT      150  
TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTTGTGAAT      200  
AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTTGAT ATACTGATT      250  
TCTTTCTTTT GTTATA      266

15      (2) INFORMATION FOR SEQ ID :896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
20      (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25      (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

AAGAAGAGTC TTCTGCACAA ACAAACCAT AGTGTGACA AATAGTCATG      50  
GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG      100  
30      GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAACT      150  
AGCAGGCCCA GAAGACCGCC CCGCCCCCA TGCCCTGGCG CAGGGCC      197

35      (2) INFORMATION FOR SEQ ID :897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
40      (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

453

## (xi) SEQUENCE DESCRIPTION: SEQ ID :897:

5 GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT 50  
GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTGTGAA 100  
TATTTTCTT CCGACTAACT CGCGCCCCAC TCTCTGCGA GCACAAACAC 150  
10 ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT 192

## (2) INFORMATION FOR SEQ ID :898:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :898:

25 TGGATGTTTT CATTGCAAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC 50  
TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG 100  
AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT 150  
30 ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT 200  
GCTCTAGTAG CCCACAGCCC AATC 224

## (2) INFORMATION FOR SEQ ID :899:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

454

## (xi) SEQUENCE DESCRIPTION: SEQ ID :899:

	GAGGTGATT CTCAGACTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG	50
5	TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA	100
	AATGCAAAAT ATTCTAATGT TTCAATGTTT TACATGAACA TATAGGGAAG	150
	CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC	200
10	CGAGTCTGGC TACTTTCTAG GTAGTGTGCT TTTTGTCAAA TTATAAAGAT	250
	ATATTCCCTT TGTTTTTTGA AAACCAGTGA GATGCTTAAA TAGAGTACAA	300
15	TTATCTCATT CAAAATGTAT GTTGTTCCT CTCGAGAATT GTGAAGGTTT	350
	TGAGATTGGA TT	362

## (2) INFORMATION FOR SEQ ID :900:

20

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
|    | (A) LENGTH: 310 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
| 25 | (D) TOPOLOGY: linear       |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30

	GTATGTAGCC CAGTGGGTGT CTTCCACAG GGTAGGTACT CAGTTTGCTC	50
	TGGAGGGTGA CTCATACCTA AACAAAGTGA CATCTCCTTT CTCAGTAAAG	100
35	CCAAAGCAGG TTTCTACATT TGAACAAAA GAGATCCTGA CCAGAGAGCT	150
	ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA	200
	AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA	250
40	AGGGAATGAG ATTGAATGTT ATTAAAGGGA TATTTCTGTC AAGTTTTGGT	300

.455

TTCTCGATGA

310

## (2) INFORMATION FOR SEQ ID :901:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15 TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA 50  
CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGACTCCTCC AAAGATTGCA 100  
GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC 150  
20 CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA 185

## (2) INFORMATION FOR SEQ ID :902:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 381 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35 ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG 50  
TCAAACAACCT AAACACTCTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA 100  
GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA 150  
40 CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTTACTT TTAGACTAC 200

456

-----  
AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAAGTCCTG TAAAGAGTAA 250  
GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT 300  
5 TGCCTTCAGA AACACTTTGC CTTTAAATAT GTGTAGCTAC AGTAAGTACC 350  
AATGGGCTAA CTAATTGAAG CTAACATTTT A 381

(2) INFORMATION FOR SEQ ID :903:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAACTG ACATATGTAT 50  
ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC 100  
25 CTCTGCGCTG TTGCGGGTCC TCGGAAGTC CTCGGAGCGG CCGTCGCGGA 150  
AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC 200  
ACTTTTTTTT TATCGGCACC AGGCCGCGTC CTCCTCCTCC 240

30

(2) INFORMATION FOR SEQ ID :904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

	CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG	50
	TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCCTAAGG	100
5	TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG	150
	CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA	200
	CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTTCAGGCTC CTGGGCAACG	250
10	TGCTGGTCTG TGTGCTGGCC CATCACTTTG	280

(2) INFORMATION FOR SEQ ID :905:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25	GTTCTAGTGG TAACTGCTGC TTCTGAAAAA TATTTAGAGA AACCAACGGT	50
	AAAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT	100
	ATTTGACACGA GTAAAGCGTA GCAAGTTTAA CACAACTTAT GTAACTTGG	150
30	AAAATTTTCC GAAATTTTAT TGACTTTTCT CGGTCTCTCC TATCTTTATA	200
	TACACATCTC TCATGCACAC ACGCG	225

35 (2) INFORMATION FOR SEQ ID :906:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

458

## (xi) SEQUENCE DESCRIPTION: SEQ ID :906:

5 GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA 50  
ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA 100  
TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG 150  
10 TCCACTGTAG C 161

## (2) INFORMATION FOR SEQ ID :907:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :907:

AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAT 50  
25 ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT 100  
TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT 150  
30 TATATATGCG CACACACACA CACACACGAC ACGACGACAC ACACACACAC 200  
TCTA 204

## (2) INFORMATION FOR SEQ ID :908:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear



459

## (xi) SEQUENCE DESCRIPTION: SEQ ID :908:

	AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA	50
5	AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC	100
	TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC	150
	ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA	200
10	CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA	250
	CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC	300
15	CAAATGTGTG TGTTTT	316

## (2) INFORMATION FOR SEQ ID :909:

## (i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 307 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :909:

	CTAGTAACAT AGAAAATAAA CTTCACTGGG AATCTCTGCT TCCCGCGTGA	50
30	GGTGTTTAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT	100
	CAAGTTAGAG GAGATGGCAG GGTCAAAATT TTAGAACTG GATCCCACCA	150
35	CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA	200
	TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCACG	250
	GGAAAAAACT GTGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTTAA	300
40	GCTATTT	307

460

## (2) INFORMATION FOR SEQ ID :910:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTGCTC AATCAAACGC 50  
AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT 100  
TAAACCGAAT CCCCACAATC TCAAACCTCA CCAGGCCAAA GGGAACACAG 150  
TGACACAACA ACAGGGTTCC AA 172

20

## (2) INFORMATION FOR SEQ ID :911:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA 50  
CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG 100  
AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAGAG 150  
AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA 200  
TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG 250

40

461

CATCT

255

## (2) INFORMATION FOR SEQ ID :912:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15 CAAGCGAATG GTAATTACAT GGTCGGATGA GGTCTCACT CTCAGGGGAG 50  
GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACTGTGTT 100  
GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT 150  
20 GCAATTTACA AGAGATTCTT TTGAAAGAAA ATAGGAAGGC AAAGAA 196

## (2) INFORMATION FOR SEQ ID :913:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35 ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA 50  
GCGATTTTAC ACTAGAGTGA ACGAACTNG AGAAGGAAAA CATCCAAGAG 100  
GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA 150  
40 TCCCACTAGG GCCACGAGAA ACAAAGCAAA TTAACATT ATCCACTACA 200

462

CGA

203

## (2) INFORMATION FOR SEQ ID :914:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15	CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA	50
	GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT	100
	AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTT AAAATAAATC	150
20	TTAGTGTTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAAATCGGA	200
	TTTCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTTT GTAGTATCTG	250
25	GAGGTGGACA TT	262

## (2) INFORMATION FOR SEQ ID :915:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :915:

	TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT	50
40	ACACGGAGTC TGTATTTTGC ATCCTAGAAT GATTAACCAG AAACAAAGAA	100

463

AGGAAAAAGG TAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT 150

AAAGAATGAA ATAATTTGAA AAAAAAGGCA GGGCAGGCAA A 191

5 (2) INFORMATION FOR SEQ ID :916:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT 50

TCCAGGAGTT GTCCTTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTGT 100

20 GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC 150

AGTGTGTGCA TATGTTTGTG TGTTGTCTC TGAGTGATAT CCACCTCTCT 200

25 CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG 250

TG 252

30 (2) INFORMATION FOR SEQ ID :917:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :917:

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA 50

464

GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT 100  
TCCTGAAGGT CATGCGATCC TTTACCCTCA GAACTTTCA GGCTGAAATC 150  
5 ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT 200  
CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC 247

## (2) INFORMATION FOR SEQ ID :918:

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

ATTGGAATC AATTGCCTGT TGCACCTTTA CATTAGTGT TGCTTAAATA 50  
AACAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG 100  
25 CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT 150  
TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T 191

## (2) INFORMATION FOR SEQ ID :919:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAGAA 50

465

ACAACCTCCT CATTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG 100

ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT 150

5 CGAACAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC 200

AACCC 205

(2) INFORMATION FOR SEQ ID :920:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTCCTC TCCAACGACT 50

CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA 100

25 CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACCGCGTT TAAGAGATGA 150

AACCACGACT TCGTCAAGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT 200

30

TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA 250

AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG 300

CTCTAAGCTA CAGGTTGATC ATA 323

35

(2) INFORMATION FOR SEQ ID :921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

466

## (xi) SEQUENCE DESCRIPTION: SEQ ID :921:

5 AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA 50  
GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG 100  
ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG 150  
10 GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCGGCGG GGATCAAAAC 200  
TATAGAAACA ACAAGTTAGA GTACAGACGT 230

## (2) INFORMATION FOR SEQ ID :922:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25

TATTTTTCCT GATGTTCTCC CTCCTCCAG TCCCGACCT CCCACAGGCC 50  
CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTTCT 100  
30 TGCCCATTTCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCTCGCTC 150  
TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC 200  
TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTGTAA 239

35

## (2) INFORMATION FOR SEQ ID :923:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



467

## (xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5	GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT	50
	TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT	100
	TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC	150
10	TGAAACCCGT CCACTCAATA AATTTTGT	178

## (2) INFORMATION FOR SEQ ID :924:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 325 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25	CAGCTGGTCC CCCACTAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG	50
	ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC	100
	AAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT	150
30	TCTTGCTTCT TGTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA	200
	GCAATCTCAT GGTCTTGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA	250
35	GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTCTGGC CTATTCATT	300
	ATTTTGGGG GATGAATTTA CAGTA	325

## (2) INFORMATION FOR SEQ ID :925:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs

468

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :925:

ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG 50  
10 AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT 100  
CCGGTTTTCT TTGTTTTTTC TCTTTATTCG TCCTTTCTCA AAGATGGGAT 150  
15 ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG 200  
AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG 250  
TTCCAGTCCT G 261

20

(2) INFORMATION FOR SEQ ID :926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :926:

GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC 50  
35 AACTGGGTTC AAATCCTGGC TCTGTCACAT ACTAGCTGTG TGACCTTGGC 100  
CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT 150  
AACCAACCAA GAGAGCTGAG AGA 173

40

(2) INFORMATION FOR SEQ ID :927:

469

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10 AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC 50  
CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TCGGCCATCC 100  
15 TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC 150  
CTTNGATTTT TCTGCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCAC 200  
TCAGATCATT ACTACTGAAC TCG 223

20

## (2) INFORMATION FOR SEQ ID :928:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :928:

GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT 50  
35 ATTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA 100  
CCACAGATTA AGTGAAGACA CCCACAATT TAATGACTCT ACGACTCTCG 150  
GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT 200  
40 CATAACTTGC AT 212

470

## (2) INFORMATION FOR SEQ ID :929:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :929:

TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT 50  
15 ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT 100  
TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG 150  
TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG 200  
20 ACATAACTTG AGTTTGTGTTG CTTGGTATTT ATT 233

## (2) INFORMATION FOR SEQ ID :930:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35 AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA 50  
GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTCAGCACA TTCATGGTTC 100  
AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA 150  
40 GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC 200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

## (2) INFORMATION FOR SEQ ID :931:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15 CTATCTAGAA TTACTTATTT CACTTGAAAT GTATGGTTTC AGGAAAATTT 50  
TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGGA ATAATGGCAT 100  
CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA 150  
20 AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC 200  
ACACACACAC ACAAAAAACA C 221

## 25 (2) INFORMATION FOR SEQ ID :932:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :932:

TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG 50  
CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC 100  
40 TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA 150

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG 200  
GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA 250  
5 ACGGAGCAGG TCAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT 300  
GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA 333

(2) INFORMATION FOR SEQ ID :933:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20

AGATTTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA 50  
GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT 100  
25 TGTTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTTCTG AATGTTTAAG 150  
AAAAAAATAA TACTTTTCAG AATTACCTAC CTCTTTCTCA TTTTTCAGCCT 200  
GGGATCAATT ATTCCCTTTC ACACTTTTTT ACATCCTAAG TAGAAATAAA 250  
30 ACTCTTTATT CTATTTTTTT TCAGTTATTG G 281

(2) INFORMATION FOR SEQ ID :934:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

473

## (xi) SEQUENCE DESCRIPTION: SEQ ID :934:

AATCTTGTAT TATGTTAATA TTAAATCTA ATAATAAGAT ACTGTAGAAG 50  
5 TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG 100  
TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAACTGTT 150  
GTTTTATCCC AAGGGTAGAG GGA CTCTAAG TAAACTGTA ACAGAATCAA 200  
10 AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGA CT 250  
TTAAATAAGT AAATCT 266

## 15 (2) INFORMATION FOR SEQ ID :935:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTA ACT 50  
ACTAATAACT CATTAAATAA ATTAATAATA TTAAATGATC TGTGTGTTCC 100  
30 ATGCAAATAA CAGAAATGATT TCCACTGAAT AGTCATGATG GTTTAAATA 150  
TTACTCTAAC ACCAATAACA ACACGTAA 178

## 35 (2) INFORMATION FOR SEQ ID :936:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :936:

5      ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGGA CACCAGAGGC      50  
TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCC ACAGCAACTT      100  
TCCCAGCCAA TGCCACGATG GAGATGACAA CCCCAGATCT GGGGANACAG      150  
10      AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG      200  
ACTTCACCCG AATTACATTT ACCA      224

## (2) INFORMATION FOR SEQ ID :937:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20      (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25

ATTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAATTGCT      50  
GGGGATGGGT AGAGAAAACC CATTTATAGT ACTTTTCTGC CTTCTTGTGG      100  
30      TTTTCGGCTT TGCGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA      150  
AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAAA CTTTTTCCAA      200  
CCAAACTCC TAAAAAACCC AAAACAGAA CAACCAATTA AACCCGACCC      250  
35      GACACAATA CCAATGACTG      270

## (2) INFORMATION FOR SEQ ID :938:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid



475

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA	150
	CTTCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
15	CTAGAACTAA AGTCA	215

(2) INFORMATION FOR SEQ ID :939:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

30	TGTCGTCCTT AATATTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTGTG TATGTTTCTA TATCTCTCTC	100
	TTTTACGCTT CTTTCCCGGA CCGTCCCTC CCTCTACAAT TATATTTACT	150
35	ACCTTCATGA TTGCTTTTTA TTATTTCTTT CACTCATCAT TATTGTTTAT	200
	TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TCGGCTTTCT CAACCCCCCT CCTTCCTCAT	300
	TAC	303

476

## (2) INFORMATION FOR SEQ ID :940:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :940:

	ACACTATTTT CAAAAATCCA AATAAAAGTG CAGTTTCAGA CTTTTTAAAA	50
15	AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG	100
	CGTTTGCATG CAACACTGCA TATTTTCTCT AATCAGATTA ATATGAGTTT	150
	TAATGTTTAG CATGAACTAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT	200
20	CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT	250
	TGCTTTGCTT TGTGGAGACT TCGCGTATT TTCTTTTGCT TGTTTGTTA	300
25	TCGCCAGGCA GCGCTGTTTC AACTGTGAGA	330

## (2) INFORMATION FOR SEQ ID :941:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :941:

	TTTATTTTCAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT	50
40	TTTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT	100

477

TTTTGCT

107

## (2) INFORMATION FOR SEQ ID :942:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15 CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTGT GTGTGTATGT 50  
GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGAG ATTTGGTTAT 100  
TTCGGCGTTA CACCTCCGGT GTTCTC 126

20

## (2) INFORMATION FOR SEQ ID :943:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTGAACAGC CGCTGGTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA 50  
35 AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA 100  
GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA 150  
AGCTC 155

40

## (2) INFORMATION FOR SEQ ID :944:

478

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT 50  
TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG 100  
GGGGGGGGTT TGGAAGCAAA CACATTTGGG GTTTTTAACC AATTGTTAGG 150  
TTCTTTTAT TTAGGGTTGT GCAGGGAAC TTTGGGAGGT TTCTTTAGGT 200  
GGGATGGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT 250  
TATTTTGTCC CTTAACTTGG TTTGTTGGGC AGGTGGG 287

20

## (2) INFORMATION FOR SEQ ID :945:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :945:

ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG 50  
TCCAATTATA ATCCCCAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG 100  
GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT 149

40

## (2) INFORMATION FOR SEQ ID :946:

479

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :946:

10

TTTAAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTAAATA 50  
AATTCACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG 100  
AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC 150  
ATTAACATTG GAAACTCCA GACCTGGACA CCAGAACCTC AAATCTGTGA 200  
GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTT 250  
TTTTTTTCCC C 261

20

## (2) INFORMATION FOR SEQ ID :947:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35

CTTTAGGAAC TGTCAGCATG TTGTTGTGA AGTGTGGAGT TGTAACCTG 50  
CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAAAGTTG CACTATTGCA 100  
AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG 150  
TCCTGTACCA GAAACATTTT CTTTATTGT TACTTGCTTT TTACACTTTG 200

40

480

TTTAGCCACT TAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC 250  
CAAGTTGTAT ATTT 264

5 (2) INFORMATION FOR SEQ ID :948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTTGA 50  
GCCAGGTGTA TTGAGCACTG GGCTCCAAC TATTGTTAAT GAGAAACGGC 100  
20 CCAACTTGGA CCATGACTTT CCCATTGCA GGTCTTAGAA TAATTTTTT 149

(2) INFORMATION FOR SEQ ID :949:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA 50  
GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA 100  
GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG 150  
40 TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTG GCACCTTCCC 200

-----481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15 ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG 50  
CACTGACAGA TTTACAGACA GGAAACAAA GCCTTACTTA CCAGGAATCC 100  
AAAGTTTATA CATGAAAATT TAAAAGGGA GTCTATGCAA AGCGGAGTTC 150  
20 AGG 153

(2) INFORMATION FOR SEQ ID :951:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35 TGCGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG 50  
TTGTTCTTAA GCGGAGCTCA GGGAGGATAC AGAAACTCT CCTGTGGTGC 100  
TATGAAATGT GGCGTAAAAA GCATTCTG 128

40

(2) INFORMATION FOR SEQ ID :952:

482

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10

GTTGGAAATT TCCCTAAAT CACCTACCGA TTACCCTTGA TTCCCTTTG 50

TTTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC 100

15

ATATAAAAT AAAGTGACC CAAATATTGT AATGTATATT GCTGCTCTTC 150

TTCAAATTAA ATAAGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC 200

AATTGATACA AAT 213

20

## (2) INFORMATION FOR SEQ ID :953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :953:

GCAGCAGTTT CTTTGAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50

35

TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100

TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAGACTAC 150

CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATT 200

40

GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT 236



483

## (2) INFORMATION FOR SEQ ID :954:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :954:

5	GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC	50
15	TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT	100
	TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAC	150
	CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATT	200
20	GCCACTGCAG AAAGTGT	217

## (2) INFORMATION FOR SEQ ID :955:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35	AGCAGCGACC GCGCTCACTG GCTTTTGTG TCTGCTGGG CCTTTTCTGT	50
	TCAGTCCATG CTTGAACTAC TCCACCCCT TAAATCCAAC GTAAAAACCA	100
	GTCCTTTCTG TGCTTGTCT CTGTGCGTTA ATGCTTTTTC TTATGCTTGC	150
40	TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG	200

484 .

TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA 250

TGCTTG 256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTCTC 50

ATTTCATTAT ATTATGGTCA GAGAATATAT TTGAATGAT TTCATTATT 100

20 AATTTTAAA AATAACATTA AAAAATTTT TAAAATGTGA ATATACCACA 150

ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA 194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50

ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT 100

40 CATTCGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGTGAG 150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA

196

## (2) INFORMATION FOR SEQ ID :958:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15 GCGCTCAGCT GGAAGTTCCG ATCTATTTTT TCTTGGTCTC ATACTCAGTT 50  
TTTTTATGTA GTCAGTTAGT AAAATAAACC TAAAAAATAA CATTGATTTT 100  
TTCTG 105

20

## (2) INFORMATION FOR SEQ ID :959:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :959:

GACAGCGACC GAACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA 50  
35 GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA 100  
TAATTCATTA AACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT 150  
TATCATGATC TGCAATCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC 200  
40 TCAGACGATG ATAAGCAAAC TCAAAAATGA AATGATGAT GCCAACTAAG 250

486

CTTTTGTTAA A

261

## (2) INFORMATION FOR SEQ ID :960:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15 CACAGTTTTG TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA 50  
TCGTTTCTTC TTTAGAGGAG TAGGTTTAA CCATGTTAAA TTTCCAAGAA 100  
TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTTC A GAAAATAAA 150  
20 TAATTTTCGA TTCAAGTACT ATACAACTT AACGATGG 188

## (2) INFORMATION FOR SEQ ID :961:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35 ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC 50  
TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTT AATCCACAGA 100  
CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTTCT 150  
40 ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C 191

487

## (2) INFORMATION FOR SEQ ID :962:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTATAT ATAAGGTTTT 50  
ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA 100  
TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC 150  
CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAT T 191

20

## (2) INFORMATION FOR SEQ ID :963:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCAGC AGGAACAGCA GCCCAATGCC 50  
TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTACACTTGA 100  
GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC 150  
CGAACACCAT CAATAACCGA ATAGACTA 178

40

## (2) INFORMATION FOR SEQ ID :964:

488

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10

ACTTTGCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG 50

GGGATCCTTT TGA CTG CAG ACGCGGGAAG GAAAGAATGA AATTAAAGAA 100

15

TATCCTTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT 150

CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC 199

## (2) INFORMATION FOR SEQ ID :965:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :966:

30

ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGATTTT 50

GGCACATCTG CAAAAGCTA CAAACAACCC CTAATAATTA CACTACTACG 100

35

ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT 150

CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTTCTCC TCGCCTTTAA 200

ACCTGCAGGT TGGGGCT 217

40

## (2) INFORMATION FOR SEQ ID :966:

489

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :966:

ATTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTTCC 50  
AATTTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT 100  
CAAGAAAAAG CAAATGGTTT AAGTTTTTAC ATAGGAAATC TAAGAACTAC 150  
TCATCAATAA AACGCAACAC TATCA 175

## (2) INFORMATION FOR SEQ ID :967:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :967:

AGGGGTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG 50  
GGGGACAAGG AAAACCTGGC GGGGGGACC GCGAAAAACA CA 92

## (2) INFORMATION FOR SEQ ID :968:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

490

## (xi) SEQUENCE DESCRIPTION: SEQ ID :968:

5           GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA           50  
          TATTGTTTCAG CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT           100  
          ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AAACCTCGAAC           150  
10          AAATAACCGA AAACCTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA           200  
          CTACTAAC   208

## (2) INFORMATION FOR SEQ ID :969:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25           AGTGGTTGCT GTTTACTGGA ATCTGTTTT TTTTTTTTCG GTTTTTTTGA           50  
          CTACTCGGGG GGTTTTTCCTT TTTACAGGA ACTAAATCAA CAAACTTTTT           100  
30          CGATTCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC           150  
          TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC           200  
          CACCAAGGAT TTAATCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT           250  
35          TTAAGA   256

## (2) INFORMATION FOR SEQ ID :970:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid



491

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

	AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA	50
10	AATAACCTAA CCCGCTTGTT TTTTCCACAC TAATACTAGG GCGAATTCCT	100
	CATTTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG	150
	ACCTAAGACA TCAGATGAAA AACAATGCCT CTATTCCTTC AAGTATAATA	200
15	AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA	240

(2) INFORMATION FOR SEQ ID :971:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

30	ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCCTA	100
	ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TGCGCGAGGC	150
35	CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT	184

(2) INFORMATION FOR SEQ ID :972:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

492

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :972:

GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA	50
TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTACTTGTTA	100
CATAATCCAG TGAAAACTCT ACTTGTTGAA ATTATGACAT AAAGATCTTG	150
CAGCTTTATT TGAGTATTGG TTCTTTTGTG TAGTTTCCAT CTTTAAAT	200
ATTTAAATA TTTTCAAGGA TAAAGTATT ATCT	234

(2) INFORMATION FOR SEQ ID :973:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :973:

TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC	50
TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA	100
AAAAAAACAT CACAAACTG AACTGCCGCC ATCACCCTA CACCAAGTAT	150
GTGATTGAAT TATTCAATGA TCTGTTTTCG CGGTAGTGAC CAACANC	197

(2) INFORMATION FOR SEQ ID :974:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs

(B) TYPE: nucleic acid

493

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

	AGCAGGAGAT TTTTSTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG	50
10	ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGACT TAAAAAATA	100
	ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC	150
	ATACAGAAAA AAACGAAATA CATAACCCCC CAGGTTTGAA AGAAAATAAT	200
15	TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC	244

(2) INFORMATION FOR SEQ ID :975:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

30	TTTTTTTTTC TGAACACTTT GCTTCACACC TTTCATATT CACGGTTATG	50
	AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG	100
	AGACCCATTA GAGATTTTCA GTCTATATGC CCAGAGCCTG ATATAATGCC	150
35	ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA	200
	TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT	250
40	TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA	300
	ATGTGCAATG AAGGGTTTCG TGTAATATTG	330

494

## (2) INFORMATION FOR SEQ ID :976:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :976:

TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT 50  
TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT 100  
TCCTTACGGC ATTCATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT 150  
AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTATAT GAATNACTTA 200

20

## (2) INFORMATION FOR SEQ ID :977:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :977:

AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTCTG ACAGGCCATT 50  
ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT 100  
AATGATGTTA TGAAACGAGC TTTGCT 3 GCTCTTGATT GGAGCTCCG 150  
GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC 3 AACTGTGTTT 200  
AATACTCTGA ATTTTAATTA GAAAAAATA CAATAGCAGC AAGGCCCTGG 250

40

495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC

296

## (2) INFORMATION FOR SEQ ID :978:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 228 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15 GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG 50  
ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT 100  
AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAGC CGGGGGAGGA 150  
20 CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC 200  
CAGCCACTAC TGATAATTCA CAACGGTA 228

## 25 (2) INFORMATION FOR SEQ ID :979:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :979:

CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT 50  
CCCCCTGACG CTAGGCCATG ACACAACTAA ACTTCAATAC ACCAGGACTA 100  
40 AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA 150

496

CCAGGCAAAA CCAGAACCTG A

171

## (2) INFORMATION FOR SEQ ID :980:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 241 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15 TGATCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC 50

CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC 100

CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTT CACACCAATG 150

20 ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATT 200

CTGCAGTGGA AAATAACTGC ACTCTCAGGA CACAGCACTG T 241

## 25 (2) INFORMATION FOR SEQ ID :981:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 base pairs
  - (B) TYPE: nucleic acid
  - 30 (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :981:

TCACTGCAAT CACGGTAGCT TCGCCCATG CCTCTTCAAC CAGGCACATA 50

CATCGAGAAG TTGAACCTGC ACTTTATTTT AACTGAACA GACTTACCCC 100

40 GACAACAACA CCTCCCCAGT GGGACAAACC TACCCACCT CCCCACACTC 150

----- 497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AAACATTTCG 200

AAAACCACAC TTCAACCCAC AGGAAGA 227

5 (2) INFORMATION FOR SEQ ID :982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG 50

ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT 100

20 CCGCGAACTC ATGACTGACC CTTCTAAGT AAGAATCCCA CCCAGGCAAA 150

CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC 200

25 AAAAG 205

(2) INFORMATION FOR SEQ ID :983:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTTA AAAATGATCT 50

40 TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT 100

- 498

CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA 150

CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC 200

5 CCCT 204

(2) INFORMATION FOR SEQ ID :984:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :984:

ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTG CATTCTTGTT 50

20

TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTC AAAATCCACT 100

AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTTGCT TTTTTTTTC 150

25

TTTCTCCCCC CTCCCCAG 168

(2) INFORMATION FOR SEQ ID :985:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 350 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :985:

CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGCCCA AGAAGCATGG 50

40

GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT 100



499

TTTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG 150  
CTGGGAGGGG GGCCCTCACC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT 200  
5 GGTCCAGCCC CTTACGCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT 250  
CCTGATGTAT TTTTTTTTCC TCCAACTCAA AAGGCAAAAA TAATCCTATT 300  
TTTATTATCT TGCTACAACT GCAACTTTCT GCCCTATAAA TTTACATTCC 350

10

(2) INFORMATION FOR SEQ ID :986:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 289 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :986:

AGCGACCGCC ACTCACTGTG AGTTCCACTT AATTCAGGTG AGCCGCTCTT 50  
25 CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT 100  
TCAACAATGC TCTGCAAATC TTTTAAAGAC CCGTTACTTC AACAACTCCC 150  
AATACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAAACCCGA 200  
30 CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAATTCTA CAAAGGACCA 250  
AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAA 289

35

(2) INFORMATION FOR SEQ ID :987:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

500

## (xi) SEQUENCE DESCRIPTION: SEQ ID :987:

5 CACAATCATA GCATTTATTA CACGATTAC ATCTGATCCT CACGCAATTT 50  
TCTTCCTCAC CAATAAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA 100  
CATTCTTTTA TTCTGCATC GCTATAAAGA AGTA 134

## 10 (2) INFORMATION FOR SEQ ID :988:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTTAGCTAT TGACTGTAGG ATTTGTAATT 50  
CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA 100  
25 ATTCCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG 150  
GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT 200  
30 TCATAATTTA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG 250  
ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC 287

## (2) INFORMATION FOR SEQ ID :989:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT 50  
TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG 100  
AATGACTCTC ACTGGCACTT TTAACACAG CAAGCCCAAC ATATTTTCTC 150  
CTTTTCATAA AGAAGCCTAT ACACCAT 177

10

(2) INFORMATION FOR SEQ ID :990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :990:

TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA 50  
TAAACTAACC CCACACCCTC ACCAACCAAA GGAGGCACAA TCCAACGAAA 100  
CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAAC 150  
CAAAAGTC 158

30

(2) INFORMATION FOR SEQ ID :991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

TAATCCCTTT TAAGCAGAGA TACACATTCA CAGAGAGAGA ATGTTTAA 50  
AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTTAAT TCATTTTGAT 100  
5 TACACAAAAA TAAGGCAAAC TAAATGATTC AGAACAATTC AATTAACTG 150  
AAGCCTTCTA GAAAAATACT CAACAGGCTT CAACAAAAG ACTTAGCGCA 200  
CATAAAACAA TCACGAAGAT CACAATTICA GCACAAATAT CTGAAGGAAT 250  
10 ACACGCAAAA CATCATA 267

## (2) INFORMATION FOR SEQ ID :992:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :992:

25 AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA 50  
TTGTCAAATT CCACTTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT 100  
CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA 150  
30 TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA 199

## (2) INFORMATION FOR SEQ ID :993:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

503

## (xi) SEQUENCE DESCRIPTION: SEQ ID :993:

TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG 50  
5 ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCGAGG 100  
AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT 150  
AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTACTGAAG ATGCGTCC 198

10

## (2) INFORMATION FOR SEQ ID :994:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :994:

GCTATCTGCG GGGCCATTCG TAGGATGGGT GAGTCAGATG ATTCCATTCT 50  
25 CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGA CTGGAGA 100  
GAATAACAGA CGTGGAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA 150  
AAAAAAAAA ACAACAAACC CCAACAAACT CAA 183

30

## (2) INFORMATION FOR SEQ ID :995:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :995:

504

ACCTCTGCAT TAACACTCCA GCACCTTTGG TTAGCCAATT TGGCCTTATT 50  
TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTTCG 100  
5 GGTTACCCCA CTGTCCCCAA CTTCGAATAT GCTCACTGCC TGGAAAATGT 150  
TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA 199

## (2) INFORMATION FOR SEQ ID :996:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20

GGTCTTGGCT GGTGGTTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG 50  
GTCCAATTTT CCACCTGGGG TTAAAAGTT AAGGAGGACC AGCCTGGGAA 100  
25 CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTTA 150  
AGGGGACACC ATATGGAGAT TTTATGC 177

## (2) INFORMATION FOR SEQ ID :997:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :997:

40

GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCATT 50

505

GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTTC 100  
AGTGAATAAT TCCTCTTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC 150  
5 GTAGAAAGTT GCTTGAAATT CTTTCTCTAA AAAAATTTAA TTTTCTATC 200  
TCAAAATGAC CGTATGCAAA CGAACATTA 229

(2) INFORMATION FOR SEQ ID :998:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :998:

20

TTGCAGTGTT TATGCCCGCC TTCTTTCACG GGCAGGTTCA ATTTCACTGG 50  
TTTAAAAGTA AGAGACAGGC TGAACCCTTC GTGGAGCCAT TTCATTACAG 100  
25 GTCCCTTAAT TTAAGGAACA AGTTGATTTA TGCTACCTTT TTGCACGGTT 150  
TAGGGTACCG CGGCCGTTAA ACATGTGTTC ACTGGGCCAG GCGGTGCCTC 200  
TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT 233

30

(2) INFORMATION FOR SEQ ID :999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

TCAAAACTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTGGCTT 50  
CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA 100  
5 TGTGGCTGGT GGGCCATGGG TTGACAAGC TTGATGTAAA TAAAACCACC 150  
AGTGGAAAGA GTTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC 200  
TATCATGATA TTAGTT 216

10

(2) INFORMATION FOR SEQ ID :1000:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

GACAAGACCT AGAAGCAACA ATGCCCAGTA GAAACAAACA CACCTACTGC 50  
25 CTGGATCTTA GTTTTAAATT ATATTCCCA ATAAAGAGAC CCAGGGCTCC 100  
TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA 150  
CCTAGAATAT CTAATACTGC CAAAATTAA GAAAGTGTC TAAAAAAT 200  
30 CCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC 250  
CCAATGGCCA AAGATCAAAT AATTTTCAA 280

35

(2) INFORMATION FOR SEQ ID :1001:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



507

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

5	TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC	50
	CTTATTTGGG GACTGGTCAC CAAAAATACC TAACTATGGT TGGAAGCTTA	100
	GTGCTTTCAG CCCCATTCCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCCC AACTCCACAA GGACCCTTCC AGACCTCACC TGTGTATCTC	300
15	TTCATCTGGC TGTTCAATTG TATC	324

## (2) INFORMATION FOR SEQ ID :1002:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

30	ATTTCATTG ATAAGTCCTC ACAAACCCAC TTTTCCTCTT GCCTGAGTGC	50
	CTCACATACC CTAAGTCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCCC CCAGTCTTGC CTGCACTCTC	150
35	CTTTCCTCCC GCAGAGAGGC ATTCCTTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCTTCC TCCAGCAAGC TTCTTAATTC	250
40	ATTT	254

## (2) INFORMATION FOR SEQ ID :1003:

508

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10

AAGGTTGCGC TGCCCATCCT CTCGCCCTC GGAATTTACC CCTGGCCGCT	50
CAGGGTCTCG CTTCTAGAAG AAGATGATGG ATACTAGGGC GATCCTCCTA	100
TTGCCTTTAT ATTAAACAGG CCCGCCGAGG AGGGGCTCCC GCTGGTGCCC	150
ACATAACTCT ATTAGACCAT CTGAGGCGAC TTCCCCCACC CCCTCCAACG	200
CGCCTCACGC ACGACTCTAG CAAAAGACAG GTTCCGCGGT GGTACGTCG	250
TTTGAGACTA TACTG	265

20

## (2) INFORMATION FOR SEQ ID :1004:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35

AAATATGCCC TGAGGATTAT CTGATGTCGA TGGTGTGGAA AAGAACTCCA	50
GCAGGCGACT TCGATTCAA TCAATGTCCC CTGAATGCCA CAGAACCACT	100
AGCAGACGCT GCTCTCTCAG TCTTAATGGA GTGGCCTTCT GGGAACAGCC	150
GAGCTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTTAA	200

40

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG 250

CCCCAGGTGA CCA 263

5 (2) INFORMATION FOR SEQ ID :1005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG 50

CTTCCATCTC ACTATTCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC 100

20 TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA 150

GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTTGGAATT 200

25 GTAAATCGT GAGCCACTCA TATTCAAAC AAAAAAGAA CAGAACTTTT 250

ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTACGGAT CAATGTCAAA 300

CGCTTGCATT CATAAAG 317

30

(2) INFORMATION FOR SEQ ID :1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTTCCTT GGAATGCCTT 50  
TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCATCCTT AACAACTAG 100  
5 CTGAGGTCTT ACCTCATCAG GATTGATCC CCCAAAAGA TTTGTCCCTC 150  
TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA 200  
TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA 250  
10 GAGTCTTTGT CTAAATACTC AAAACCCTGT TTACCAT 287

## (2) INFORMATION FOR SEQ ID :1007:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

25 GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA 50  
CTGTCTCATC GGGGCACTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA 100  
TGCTGTATTC AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG 150  
30 TAAACTTTGA AGCCCTTTGA AGGACCTAAC CAAACAACAC AAGGATGAAA 200  
ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA 250  
35 TATTCGGATT TTACCGTAAG GAA 273

## (2) INFORMATION FOR SEQ ID :1008:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 308 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT 50  
TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC 100  
10 CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT 150  
GCGCCCTCTC CCTGCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGGCA 200  
15 TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG 250  
GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG 300  
CAAAAAAA 308

20

(2) INFORMATION FOR SEQ ID :1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

GAACCGCTC TGTTTCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA 50  
35 GCAGTTTTGA AACTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA 100  
GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAATAA TGAGTGTAC 150  
TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA 187

40

(2) INFORMATION FOR SEQ ID :1010:

512

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10

AAGAAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG 50

ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA 100

15

AAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAAAT 150

AAGCTACTTC TCCTTGATAT TACCT 175

## (2) INFORMATION FOR SEQ ID :1011:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

30

TGAAAAATAT TTGGAACCTCT TTAGTACAGA ACAGTTTCAA TATGAGTTAA 50

GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA 100

35

CAGAAGCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT 150

ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG 200

TATTTTAT 208

40

## (2) INFORMATION FOR SEQ ID :1012:

513

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10

ATGATATCTA GACTACCACT ATTTTTTGAA TGAGGCTTC TTAGGAGTAT 50  
GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG 100  
ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG 150  
ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA 184

15

## (2) INFORMATION FOR SEQ ID :1013:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30

CTTTGACATT TGATCAGACC AAACAGTGCT GTTCCCGGG GAGGAAACAC 50  
ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC 100  
ATACCTTGTT TATCAAATGA GCGACTCAAA ATGATTAAAA ATAATGCTGT 150  
TCTTTAGTAG CAACTAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC 200  
CGGAAAGAAG CATTTTTGAT ACTTTACTGC GAGTCAAAAA TCAATACGCA 250  
GAATGGCATT TGA 263

40

514

## (2) INFORMATION FOR SEQ ID :1014:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

	CAAATTAAGT GCCAGAATGA TGCAGCCCGC TCTCACCAGG AAGAACGACA	50
15	TGTGAGAAAA CTTATAGCAG ATGCAAAAAT GTCAACCCAC CATGTTATTT	100
	AAAAAAAAAT ATGACCAGGA TACAAGGACA CTTACCCGT TTTAACCCAC	150
	ACAAGGTCAG GTAATGTTTA CCTTGAAACA CAATCGCATA TGACCCTTTA	200
20	TGCCACTCAC CTAGGCCTTT AATAATGAG	229

## (2) INFORMATION FOR SEQ ID :1015:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

35	GAAATAATG ATTCATATTA CCGGGTATTT CTTATCCAGT CTTTCATTCT	50
	ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG	100
	TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC	150
40	ATGCACATAT ACACACACTC ATAGAGAACA AAATTATTCC GAATATTTCA	200



515

TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA

246

## (2) INFORMATION FOR SEQ ID :1016:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15 TTCATAATCG CTGGCACTGA ACAAAGTTGC AGAATTCTTT GCCAGGTACT 50  
TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC 100  
AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG 150  
20 ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA 200  
GAATTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC 250  
25 AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA 287

## (2) INFORMATION FOR SEQ ID :1017:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 299 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA 50  
40 CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTGAA ATGCTGTTTG 100

516

TCAACATTTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG 150  
TTAACCACAA TCAGTTCTAC ATAATTTAAC AGAAAACATC TGGTGGCACT 200  
5 TTTAAATGTT TAAGGACAGC ATTTACAAA CTAAGCCCCG CCCCAGTCCC 250  
ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA 299

(2) INFORMATION FOR SEQ ID :1018:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

20

ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT 50  
GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT 100  
25 TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG 150  
TGGGTTTGAG GTGGGCCCAA GAATTTCCCT TTTTACAAG TTCCCAGAAG 200  
ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTTT 250  
30 AAGAGGACAA TCTAAAGTGC TCCC 274

(2) INFORMATION FOR SEQ ID :1019:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA 50  
5 CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC 100  
GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG 150  
CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA 200  
10 AAATGGCACC TCATCTTTGA TCRAAGATTG AG 232

(2) INFORMATION FOR SEQ ID :1020:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25 AACAGTCCAT GCTGATCTTA GTAACATGA TGAAGATGGT GCTTGGCCTG 50  
TTCTTCTTGA TGAATTTGTT GAGTGGCAAA AAGTCCGTCA GACATCATAG 100  
CAAGAACTAT GTGAAGAAAA TGCAACCTT TAC 133  
30

(2) INFORMATION FOR SEQ ID :1021:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 280 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT 0  
ATTTAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG 100  
5 ACTGTTGAAA GTTTAAGTAT TAGTAACTT GAGTTACTTT TTCTTTCAAA 150  
TTTCACTCCG CTTCCCTGCA TTTCGAAGCT GCTCTTCTG GTCCTACCCA 200  
CCACCCACCC AACAAGACTT GTGTTTGTTA ATAGAAATAA TTTATCAAGG 250  
10 TATTGGGGAT CCATTGTCTA TATTTAAAC 280

## (2) INFORMATION FOR SEQ ID :1022:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

25 AAAATAAATA ACTTCTTAGA TTTTGGACTG AAAAGATCTG AGAATGTTCT 50  
GCCAAACAGC CGACCAACTG GTGCAAAGG TTAAGGCTGA CTTGACTTAG 100  
CAACCTGCAG CACAACCAA AACACTGATG CAGTTCAGAG CTCTTCAAAT 150  
30 GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA 200  
ATCCTCTAGA CAGTTTTCTT TTGTTTTGC ATGCATCCCG TTCCATTTTC 250  
ATTACGGGCA TCTATTCCTT GATCAATTAT GTGCTTTGCT TTTAATCGG 300  
TTTT 304

## (2) INFORMATION FOR SEQ ID :1023:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs

519

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA 50  
10 CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC 100  
GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG 150  
15 CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA 200  
AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT 237

20

(2) INFORMATION FOR SEQ ID :1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

30

GGCATGATTA TTAGAACTA TTAAAGCTTT TTTCTTTGAA AAACAAGCTC 50  
CTTTTACAGA ATATAACAA CAGTAGTGCC TGTGGTTTAG CCCACCAATC 100  
35 TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT 150  
TTTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAATAG ATAAAAGTGG 200  
TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT 250  
40 TTCACTTGTT TAGTTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT 300

520

TAGAGCCAAC AGGAATCTGC

320

## (2) INFORMATION FOR SEQ ID :1025:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15 TTCTGGCACC ACATTCAATA CTGATTCACA GGGATCTAAA ACATTCTAGT 50  
TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA 100  
ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG 150  
20 TTCCACAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT 200  
CT 202

## 25 (2) INFORMATION FOR SEQ ID :1026:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

ATTGGTAGAC AATATCATAA GAGTTTTCTG ATAAAAGATG CTTTTTAACC 50  
CTGACTCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA 100  
40 AACTTATACA TTTCATAAAC TAAAGGTCAT CCAAACACTG CCAAAAACGT 150

521

TTTTATAAT TGAGACCTAC TTACATCACA TCGGTTTTC AAAGAGAATA 200

CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA 243

5 (2) INFORMATION FOR SEQ ID :1027:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTTCCA ATGCACAGTT GCCACATTTA 50

GTCCTGACTG TAGGAAACAC TGATTTTGTA AAGTGCCTT TATTTGCTGT 100

20 TAACTGTTAA CTATGACAGA TATATTTAAG CCTTATAAAC CAATCTTAA 150

CATAATAAAT CACACATTCA GTTTTAAAAA AAAAA 185

25 (2) INFORMATION FOR SEQ ID :1028:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 312 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC 50

T TAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG 100

40 AGCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG 150

- 522

TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG 200  
TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCCT TCTCCTCAGC 250  
5 CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT 300  
CTGTTACAG TT 312

## (2) INFORMATION FOR SEQ ID :1029:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

20

ATTATTATA AATTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT 50  
TTGAATTCAA ATTCATTCAA AAGTTGCACA AATTATTTC TTTTTCCTG 100  
25 AACATTCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT 150  
TAAGAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATTT 200  
TATACAGATG GAAAAAGA 218

30

## (2) INFORMATION FOR SEQ ID :1030:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1030:



523

TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTTAAAC ATTGAATAAA 50  
ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT 100  
5 TTCTTAGTTC TTTGGACACA TCCG 124

## (2) INFORMATION FOR SEQ ID :1031:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTTCAGTC TGTAGCTTGC 50  
20 CTTTTTATTT NTTAATGGGT ATCTTTAAAA AAATGGAAGT TTAAAGTTTG 100  
AATGGAATTC AGTTTGTTTT TAAAGCTTGT GCTTTTGTG TTCAACTAAG 150  
25 GGATATTAGC TTACCATTTT TCTCGGTTGA ATATTATGTG TTTATAGACA 200  
AGAAATGGTC ACTAAAGCAA AATAACTGAA AATTATC 237

## (2) INFORMATION FOR SEQ ID :1032:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1032:

ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCCGAGT TCTAAGGCCA 50

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA 100

GCGACTTCCT TGAAGACTGT TTTTAACATA CCAAAGGAGG ACAAGCT 147

5 (2) INFORMATION FOR SEQ ID :1033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double.

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA 50

GAGGGGGGCA CTAGAAGCAA TATCTCCGAA ACTTCTTCGA CTGTCGAGAC 100

20 TTTTACTCA TAATTCGCTT CAAGCCAACT ACGGAGGCGC ATTTACAAA 150

CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA 200

25 TCCTCTGTCC CTA CTCTCCCTC TCCTAGGACA CCGCATTA 238

(2) INFORMATION FOR SEQ ID :1034:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT 50

40 GGACTGTGCA GGG 63

525

## (2) INFORMATION FOR SEQ ID :1035:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCGC TCAATGGCGA AATCCGAGC CAGAGCTATT GGTGAATGA 50  
GTAGCGCTGA TGGTTTAGAT AATACTAGT ATGGGGATAA GGGTGAGCAG 100  
GCGCGCCTTG AGGCAAGAAG CGGGTTAGAG CATCTCTACT TAAAAGCCA 150  
AAGCCTATAA CGGTAGCGTC TACATCACGA 180

20

## (2) INFORMATION FOR SEQ ID :1036:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA 50  
CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA 100  
CAACGGCGAC ACTCGACTAA CCATTTTAAA CCAATTGGAA CC 142

## (2) INFORMATION FOR SEQ ID :1037:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs

526

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC 50  
TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG 95

10

## (2) INFORMATION FOR SEQ ID :1038:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT 50  
TTGACAAAAA CATAACACA TAGTACAGGT AGAACATATA ACTGGTTGAT 100  
GCTAAATAAC AGATCCAGAT AATTTTCAAT TTGAATTAGC AGCAGGGAGT 150  
CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT 195

30

## (2) INFORMATION FOR SEQ ID :1039:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

527

(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

	GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAAGACAT	50
5	TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTT TAAGATGAGG	100
	TTAAGTTTCT TAACAAAAGA ATAAACAAC GTGACTCTAT CTGTCGGGGG	150
	AGGGTCTAGA CAGAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA	200
10	CGAGACTTTG ATGGAGAC	218

(2) INFORMATION FOR SEQ ID :1040:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 318 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:

25	TTTATTATTT TGAATGATTT AATGGTTTTT TACACAATTT ACATCACAAC	50
	ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATTC	100
	CTTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG	150
30	CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTTAAAGATG	200
	CAAATGCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA	250
35	CAAGTCCTAC AATTTTAAAA AGGCTCGATG GAAAAATTC TCAATCCTGA	300
	AATCCCCTAG GGAAGGGG	318

(2) INFORMATION FOR SEQ ID :1041:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs

528

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA	50
TGCCGCCGAG GCGGTGGACC GCATCAGGTT GCGCTGACG AACGCGAGAT	100
TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC	150
TCTCCCTGTG AGCGGAGGTT GGGGGGCCGA TCTCCCGCCG GTGCCGGGC	199

(2) INFORMATION FOR SEQ ID :1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

GCCTCTAACA AAAC TAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC	50
CTTTATACCA AGAAGGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG	100
CCCAGGCAGA CTTGAGGGG TTCGTGCTGT AAGACCTAAA GTTCTTATAG	150
ATTGTCCAAA ACAAAGAAAC ATGTCAGCAG GGCCTATGGT GGTTCATGT	200
GTGCTAAATG TGTTCTGAC AGGATCAAGC GTGCTTTCCT TATCGAGGAG	250
CAGAAAATTC GTTGTGAAAG TGTGAAGGC ACAAGGCACA ATGTCTGGAA	300

40

(2) INFORMATION FOR SEQ ID :1043:

529

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

10

GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAGAGA 50

GTCTGGGATG AAGCGGCCTC CTCCTGTCT TGCCCTCCAA AATTGAGTCT 100

15

GGCCTGATTCTTTGAGGAG CAAATTTTAC AATCATCCCT CACCCTAACA 150

CACGGTGAAA CTGAAAACC 170

## (2) INFORMATION FOR SEQ ID :1044:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

30

GGCCCCCCT GGGGACTGCT GGTTTCAGG GGCCACCCC CCTCATCCAA 50

AAGAAGAATC AAGTTTGTGTT TTCCTGTGGT TCCCTTGCTC TCCCCGGCCT 100

35

CACCTCGAGC TTCCAATTGG GCCCTTTCCC ATGCTTCTAC TTGAGCCCCG 150

CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT 200

GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCTAT 250

40

TTTTTTTTTT 260

530

## (2) INFORMATION FOR SEQ ID :1045:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA TTSTAAGGGC TTAACCTGTG ACTTTAATAA GCTGGAACAG 50  
TCCACTGAAT GGGTATAATG AATTGCAGTA TATACGTATG ATCGCTTTTT 100  
AAGTGATTAT CTTTTCTTTC GTTAAGTCAT GTAAATTCAT AAATTTTTTG 150  
GCACTGATGT GTTG 164

20

## (2) INFORMATION FOR SEQ ID :1046:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

TCCCTCCTTT CCGAACTGGA GCCCCATCCT CTCCAGAGTA TCCAGGGCTT 50  
CTTCACTCCC GGGTACCTGC CCTTCGGCCC CTTTTCACCA CAGCTGTGCT 100  
ACTGTCAACC AGTCTTTGCT GCATAGGCAT 130

35

## (2) INFORMATION FOR SEQ ID :1047:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs



531

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

10 GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC 50  
AGTGAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTTGA 100  
CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG 150  
15 TGAATCTCCA TTCGAGGAAG GGGAAGAAGA GCTCGGAGGG TGACAGCCTC 200  
CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCTT CTCCTCCTG 250  
ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA 285

20

## (2) INFORMATION FOR SEQ ID :1048:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

TAAAACTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA 50  
35 CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC 100  
CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC 150  
GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC 200  
40 CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA 233

532

## (2) INFORMATION FOR SEQ ID :1049:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

ACTTTAATTT ATTTCCGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC 50  
15 TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG 100  
AACTCTGAGC TGTCCCTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC 150  
TTAATTCCTC ACGACTCAGA AATGTTAACG GCACTGTCGA GTGCTGTGAT 200  
20 CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTT 250  
GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTCGGTCGA TAC 293

25

## (2) INFORMATION FOR SEQ ID :1050:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

AAACTATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA 50  
GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTTGGCA GATAAATACC 100  
40 AGATCAAAAG TCCTGTTTCA GTAATTTGAT TAAACTGTAG AATACTAAAA 150

533

AATAAGTTAT TTCTACAGAA ATCTTTGAAG GGAGCAAAAA ATCAAATCAC 200

AGTATATACC TAATGGCTA 219

5 (2) INFORMATION FOR SEQ ID :1051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATTCCTGTC AGTCTTTGAT TTTTCGTTTT 50

TGCGATAGTT TACTGAGAAC 70

20

(2) INFORMATION FOR SEQ ID :1052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTCAAGA ATGGTACCTC 50

35 CTGCCGATGA TTTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC 100

CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTTTA 150

TCTCAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG 200

40

TATT 204

534

## (2) INFORMATION FOR SEQ ID :1053:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

ACTAAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT 50  
15 AAGAGAGGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG 100  
AGGTATAAAA GGTATCCAAG AAAACTAAAA CATACAAAGG CAATTCAAAT 150  
CRAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC 200  
20 CATACCCGAC AGAAAGTACC GGAATACCAC CGACACTGAT GTCTTCCAAA 250  
CG 252

25

## (2) INFORMATION FOR SEQ ID :1054:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA 50  
CATCTGCTTA TTAAACACTG AAGTAAAAGA ACTAATCCAG TTGCGAGTCT 100  
40 TTAGAGGTGT TTAGTATTTT ACTCCGTTCT GATGGAAGCA CTTTGAATGC 150

535

TTGCATGGAG ACATAAACT GAATATTTAA TTGACAATAG ATCATGCGCC 200

TGTATTTATA AA 212

## 5 (2) INFORMATION FOR SEQ ID :1055:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double.  
(D) TOPOLOGY: linear

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

ATAAACTGTG CTAATAAAG TTTTATTTTC ATCAATATAA AAGCTGTAAA 50

AAAACCTGAGG AGAAAGCAGT TGCCAAAAG ATGAAAGAAA AACAACATAG 100

20 AAAACCTTTA AAACAGGCAA AAGTCAGTTC ATAATAAAGT AACTCATCTC 150

AC 152

## 25 (2) INFORMATION FOR SEQ ID :1056:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGT 50

GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG 100

40 AGATGTTGTA GTCGGAGCCT CATTCTTCC GGGGCACTGT TTCTTCTAAT 150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG 200

GCAAA 205

5 (2) INFORMATION FOR SEQ ID :1057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC 50

CCTTTGTCTG TTAAATACA CTGGGAGCCA GAGCTGATTC CCCACCTGCT 100

20 GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT 150

GATAGCAGGT TTAAATGA ATCC 174

25 (2) INFORMATION FOR SEQ ID :1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA 50

GCTTTAAAT ACCATGTTGA CAGCATTTTG AATTGTTCA TAGACGTACT 100

40 TATTTAACTG ATGCGAACAT TCACA 125

537

## (2) INFORMATION FOR SEQ ID :1059:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTTCA AATACTGTCT 50  
TAGTATATTA AACTCTTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC 100  
GTTGAAAACT TAGGTTTGTT CCTTCTAAAA TTTCTAAGTC CTCATTATG 150  
ACTATAAAGA AAAAAGGTTT ATCAATTCAA AAAAAATCC TGATTCTTCA 200  
AAATA 205

## (2) INFORMATION FOR SEQ ID :1060:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

ATCTCACAGA TTCTTTTTC AAGATTCATT CATGTTGAGT GAAAGAAGCC 50  
AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTTG 100  
AAACTAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG 150  
GTGAGTGTCA TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT 200

538

ACTTGGATT TGGGTCTA 3CTGGCAGG GGAAGGATA CATTGCAAA 249

## (2) INFORMATION FOR SEQ ID :1061:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

15 TAGCACATTG CATCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA 50  
AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT 100  
GCAGAATCAG TGGTTGAAAA AGGAGAAAGA GAGATTTTCT TTACAAAAGC 150  
20 TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC 200

## (2) INFORMATION FOR SEQ ID :1062:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

35 GCGCACAGCT GACAATCTCC GGTCTTGTCT CACTTTGGAC TGGGACAGTG 50  
GATGCCCATC TAAAAGTTAA GTGTCATTTT TTTTAGATG TTTTACCTTT 100  
ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG 150  
40 ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTTCCT 200



539

## (2) INFORMATION FOR SEQ ID :1063:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

TATCAAATCA TGAGTTGAAA GATTTTGACT ATTGAAAACC AAATTCTAGA 50  
ACTTACTATC AGTATTCTTA TTTTCAAAGG AAATAATTTT CTAAATATTT 100  
GATTTTCAGA ATCAGTTTTT TAATAGTAAA GTTAACATAC CATATAGATT 150  
TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC 200  
AAATTCAAAT CTCAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA 246

## (2) INFORMATION FOR SEQ ID :1064:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

CCCTCATGTG, CCAGTTCGGT CTGCCTGCAG AGGCTGTGGA GGCCGCCAAC 50  
AAGGGCGAGT GGGAAGCGTT TGCAAAGCCA TGCAGAACAA CGCGCAAGTT 100  
TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA 150  
TGGAGCCTGG ACTGAGCCAC 170

540

## (2) INFORMATION FOR SEQ ID :1065:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTTCATT 50  
GACCTCTGTG TGTCTTCAGT CCTTGACCCT TTAAGGCTCC CTGGTGCCAG 100  
AATGTCTGCA GCTGTAGGAT CAAAGACCCT TGGGGGAAAA ATCCATTCTC 150  
AAAAGAGAGG AAGATGGGGT G 171

20

## (2) INFORMATION FOR SEQ ID :1066:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT 50  
ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAGC 100  
TCATACACAG CTTTCATGGGT TTACTTTCCC AAGCACTTCC TCCCTCCCTG 150  
CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTTCC CCTTTTTCAA 200  
C 201

40

541

## (2) INFORMATION FOR SEQ ID :1067:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT 50

15

GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG 100

GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG 150

C 151

20

## (2) INFORMATION FOR SEQ ID :1068:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTTG 50

35

ATCTGTTTGC TCCTTTGAGT CTCCTTTTTA CTTTACAAC AGAAAACCAA 100

TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC 150

TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTTA 200

40

AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTGGAA 250

542

ACTGACTTTA AAGAAAACAT ACA

273

## (2) INFORMATION FOR SEQ ID :1069:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15 CAATCTTGCT TATAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCAT 50  
TCCTGGTGCA ATTGTGATTT TTTTITAGCC AAAATGAATG GCRAACTCTA 100  
TTTAGAGCAA AGTAAGTATT AGAAAACCCT AGGAACTCTT AATCAACGTT 150  
20 TATTACACTT TTATAAAGGC AACTACGCG AAAGAGCCC 189

## (2) INFORMATION FOR SEQ ID :1070:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35 TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT 50  
TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG 100  
TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC 150  
40 ATGAATCACG ACTTCTCATC CCGTTTATC AGAGTGCATA TACGTCCTAC 200

543

TTAAGGAAAA GTAAACAGT CATTTACGAA AGAAAGTCAA TCTGTATCCT 250

AAGCATTTTA ATAAAAAGTC AGAAGGAATT 280

5 (2) INFORMATION FOR SEQ ID :1071:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC 50

TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTTGAAA 100

20 GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA 150

GATGCGCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG 193

25 (2) INFORMATION FOR SEQ ID :1072:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCAGATA GGCCACGCGC 50

AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC 100

40 CACTCTGCAG CCATAGGCCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG 150

544

TCAAGTTCCC CTCGAGATTC ACATC

175

## (2) INFORMATION FOR SEQ ID :1073:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15

AGTGCCCTAC TCTTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG

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GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG

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GTGGACAGGC TAATTTTCC TTGAAAATGT GGCTTCTTCA ACTCCTTTCA

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AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT

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TCTCTTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA

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25

TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA

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TCTATATAGC ACATAGTGTT TAAAGACTAA TGAATGCAA

339

## (2) INFORMATION FOR SEQ ID :1074:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1074:

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ATTAATTATG CGGTCCTCCT CCTGGCAGCT GGACACCACT TTGAATCTTC

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CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA 100  
ATCAAGAAAC TCGGACCCAA CTTGGTGCAA AGACGGATCT CCGCCGATTC 150  
5 TGACGGCTCT CCAGGTTTTG TC 172

## (2) INFORMATION FOR SEQ ID :1075:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

AGAGTAGGAA GAGGGAGGGG AACAGGCATC TAAGATAGAC TTTCTCCATC 50  
20 TGTGGGAGC CTGGGCAAGT AGGAAAGAAG CCTTTTTCAT ACACTTCAGT 100  
CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGCGCAG 150  
25 CCTGCAAATG AGACCACTCT CATTCTCAG TTTCGATTG ATTCACTCAC 200  
TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG 250  
GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACGTTG CTACTGATG 299

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## (2) INFORMATION FOR SEQ ID :1076:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

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GCCCTCATCG GCGATACTGG AGGTTGCTT TCTCAACCCT GTGGGCTTCA 50  
CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC 100  
ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG 150  
AATGCCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG 200  
CGAGGTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA 250  
TCATTGGAAG TATTGCTATG AGCAGTCCGA AAA 283

## (2) INFORMATION FOR SEQ ID :1077:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 297 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

25 ACCAATCAAG TACTACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC 50  
AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAACTC GAATAAGAAG 100  
TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA 150  
30 GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA 200  
GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTTCAGGC TGGAAAATA 250  
35 TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC 297

## (2) INFORMATION FOR SEQ ID :1078:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



547

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

AATCTTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC 50  
AGTGATTGAA CCTTTATTAT TTACCAGCTA ATATAGTAGG CCCATAAATA 100  
GGTTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG 150  
TAGCGCTACT ACCCATACCT GCTAGCAGTC AAGGTTGAGA TAATCATAAC 200  
ACGCCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA 250  
GTTTATATCT AAAGCCCATG TTCTTTTGCT TAATATTAGA G 291

## 20 (2) INFORMATION FOR SEQ ID :1079:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1079:

AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAC ATAAGCGGGG 50  
CTCACTCACC CACCACATTA ACACCACGAA ACGGGTAATC TAACACGAGA 100  
AAACACCCTA ACGTTCATAC ACCCCATACA CCATTA 136

## (2) INFORMATION FOR SEQ ID :1080:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT	50
GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA	100
10 GCTGCGGTAT TAAAAAATC AAGAATGGAA GCGTTCCTCA ATTGTCGTTG	150
AGAATCATAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT	200
15 CGCGCGTTTT TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA	250
CACATTGGAG TCACGCGGCC TGCSTAAGAG TATGAAGGTC TTCCTGTAAA	300

## 20 (2) INFORMATION FOR SEQ ID :1081:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

30 GTTAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA	50
AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT	100
35 ATTGGATGAG ATTTGTTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC	150
TGAAAATCTC TAGACATTTG CTGAAATTGA TGAGAGCATG CACAGGACGA	200
CTGAAGGTGC TGGACATGA	219

40

## (2) INFORMATION FOR SEQ ID :1082:

549

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

10

ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG 50

AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG 100

15

CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT 150

GCAGCACAGG CGTGATCCT CTCCAAAAG CTGCTGCTCA TTTCTGGCCC 200

CATCTGCTGC TATCTTTGCC AGTCAGCCAT CACAGTTTGG CATCATCAGA 250

20

GTCTCAGCTA GAGGGAGCGT GTCATTCTG CCTTAGTGGT TTGCCTGCGA 300

CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACCT 350

25

GTCGGAAGTT 360

## (2) INFORMATION FOR SEQ ID :1083:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT 50

40

CTTTCAATTA AATACACTCC AAGACATCGA GTTGGCAGA TATTGCGCCC 100

-550-

GCCGTTTTGC TCTTCTTATC TTGTATCCA GCCAAGCCTG AAAAGTCTCT 150  
AGACATTTGC TTGAAATTTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT 200  
5 GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAAAAA AAAGTTCAG 250

## (2) INFORMATION FOR SEQ ID :1084:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

20 TNCTAGATAC NTCCCTCTGT CTCACATTCA TAGTGTGTTT TGTCTAGTG 50  
TATGAAGTCT CACNCAAGGA AAGTGTNCAG GCAGAGTTTG GGGAGAGTGA 100  
AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG 150  
25 GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTAAA 200  
AAATTAAAAA GAGGATTTTT AAAAGGAATA TCTTGTTCAA AATTNTTAA 250  
GTTTAAATAG G 261

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## (2) INFORMATION FOR SEQ ID :1085:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

5 GCAATCCATA AGTGTCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT 50  
CTTCATGATC TTTTTCGATT TTAAATGTC ATGCAATTTT AGAGAAAAGC 100  
TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA 150  
TCACTTTTTC ACTTTCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC 200  
TTAATACACC AGACAAGAAC AACTATGAA TCGGAGACAG AGGGAGACAG 250  
10 AGGCGAAATA 260

(2) INFORMATION FOR SEQ ID :1086:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

25 AAGACGTGGA TTGCTGGAA GACACGGATT TCCTGGAAGA CCTGGATTTT 50  
TCGGAAGCTA TGGATTGAG GGAAGACAAG GATTTTCTGG AAGACATGGA 100  
TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA 150  
30 CGAATTTCTT GGAAGACCCG GATTTTTCGG AAGCTATAGA TTAAGGGAA 200  
GACAAGACGG ACT 213

35 (2) INFORMATION FOR SEQ ID :1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

552

## (xi) SEQUENCE DESCRIPTION: SEQ ID:1087:

5 TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG 50  
TTTAGGCATT TGGAAAATCT GGTTCACATC ATAAAGAACT TGATTGAAA 100  
TGTTTTCTAT AGAAACAAGT GCTAAGTGTA CCATATTATA CTCGACGTCG 150  
10 ATCATTCTC AGTCCTATTT CTCAGTTCTA TTATTGAGA ACCTAGTCAG 200  
TTCTTTAAGA TTATACTGG TCCTACATCA AAATAATAGA AATTACGTTT 250  
TTTTTT 256

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## (2) INFORMATION FOR SEQ ID:1088:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID:1088:

TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC 50  
30 TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCCAGACAG GGAGACCAGG 100  
GCTCTGACAG TGACAGGTTT TTCCCTCTGA AAAAAGAATA GAAGAGGAGC 150  
TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA 200  
35 AACACAGAAG AGAGTGTGTC TCCCCAACC TCTACCAGAC AGTAGAGAAA 250  
CTGAGGCGAG AGGC 264

40

## (2) INFORMATION FOR SEQ ID:1089:

## (i) SEQUENCE CHARACTERISTICS:

553

- (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1089:

10	GACCTGGAAT TTGTTTTCGT CTGTTTCAGTA GACTCCGATT TCAGAATATG	50
	TCGGAATTTT AGACTCCGGA ACTTTTGAGA ATGTCATTAC AGGAACTTTG	100
	TTTACATACC GAGCTGTTAG CCCAGTCAC TGGGTCCGAA ATTACGCCGA	150
15	TACCGAC	157

## (2) INFORMATION FOR SEQ ID :1090:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1090:

30	GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA	50
	CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT	100
	AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAAAC TCGATGAGAGA	150
35	GAAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTTGGT	200
	CAAGTAATGG AAAC TTTTGA CTACTAGTGT AAGTCAAAG ACAAAGGACT	250
40	CCAGCAAGAT GAGAGATTTC TCTATTTTGT AACGAGTAGT CCACCGATCG	300
	TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAAAA	350

554

AAAAAACATA GATGTT

366

## (2) INFORMATION FOR SEQ ID :1091:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- 10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15 GGTCTGAATC ATGAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC 50

AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTT GCTCTTGTC A 100

CACCATATGA AGACATCAAA AAACACTTAA GGATTGAGA AAGAGAACAT 150

20 CTTTGTGTTAA AGAAGAGAAT AAGATTTTGG AAGAAAAAGT AATAGCAAAT 200

TTGAAGAAGA AACAAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA 250

25 TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTG AAGAGCAAAT 300

GGACA 305

## (2) INFORMATION FOR SEQ ID :1092:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 237 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- 35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1092:

40 AAATGGAAGT TGAAGTGAAGT GTGGTTTCCA GTACAGGGCA TCTGGCCACC 50



555

TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT 100  
GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTTG 150  
5. CTTCTTTATT TTTATTATTA TTATTTTCT TTTGTGGAG AACAGCGTCT 200  
TGCTGTATTG CCCAGCCTGA TCTCAAATC CTGGGCG 237

(2) INFORMATION FOR SEQ ID :1093:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 420 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

20

AGAAATTAT TGCCTCACAG TTCTGGAGCC TGAAGTGCA ATATCAAGGT 50  
GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA 100  
25 GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA 150  
CAGTCTTCTC CATGTGTATC CTCCTTCAG TTTCCCTTAT AGGACACCAG 200  
TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTTGA AGTTACTCAC 250  
30 CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTA GGAAGTAGGA 300  
CTTAGGGCTT ACAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTTA 350  
35 AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATAACACA TTAAGGTTTG 400  
TGGGATTGAG AAAGGTATAC 420

(2) INFORMATION FOR SEQ ID :1094:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 base pairs

556

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

5 GTTTCTTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA 50  
10 CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTT TCCATAGGAG 100  
GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC 150  
15 AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT 192

(2) INFORMATION FOR SEQ ID :1095:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 228 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT 50  
30 ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCTCCTCCC 100  
ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTTT CACCAGCATT 150  
35 GCCAAACCAC TTGGGATTCC TGC GCATGGC TTTGCTTAGT TTGCTCTTCT 200  
GCTTCTTGGA TACCTCCTTC AGGAAATC 228

(2) INFORMATION FOR SEQ ID :1096:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs

557

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID :1096:

ATTTTTTATG	GAAAAAGGGG	GATAATGCAA	AATAGCAAAA	ATTGTAAACA	50
AAGTTAAAGA	TTATCTTCAT	CTAAACCTTA	AGCTGACAAT	TTAAACACC	100
TTGTGCATAA	TGCAGAAAAA	AACTGTCCGT	TTGACTTCAC	TTTCATTAC	150
ACTGCTCCCT	ACGCATGAGA	AAGACCAGAT	GTCTGGTTTC	AGAGTATT	198

## (2) INFORMATION FOR SEQ ID :1097:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1097:

TAGAGAGAAG	TTGATATATG	AAGATAGGGT	GGACAGGACT	GTGAAGGAGG	50
CTGAAGAAAA	ACTGACTGAA	GTGTCACAGT	TTTTTTCTAC	AAACTGTGA	100
CACTTCAGTC	AGTTTTTC				118

## (2) INFORMATION FOR SEQ ID :1098:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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558

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

5      AAACTGACT AAAGTCANTG TGTAATACGA AAACCGAACA CTCCAGCAGT      50  
CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNGGGACTCG      100  
TCNCAGGTGT TTNGNACTTG CCGCCCCGACN GGCNAAGG      138

## 10      (2) INFORMATION FOR SEQ ID :1099:

## (i) SEQUENCE CHARACTERISTICS:

- 15      (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20      (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

ACTCCACCAC TGGGNCCGCC ATGTTTTGGG TNGGNGCAAT GCGCTGTCTG      50  
TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT ACACTGACTG      100  
25      ACACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG      150  
G      151

## 30      (2) INFORMATION FOR SEQ ID :1100:

## (i) SEQUENCE CHARACTERISTICS:

- 35      (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40      (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT      50

559

CGTGTAAGTA CACTCTATAT TGGCACAACA TAAAATTAAC TAGTGACGCA 100  
TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT 150  
5 CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG 200  
C 201

## (2) INFORMATION FOR SEQ ID :1101:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

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TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT 50  
CGTGTAAGTA CACTCTATAT TAGCACAACG ATAAAATTAA CTAGTGATGC 100  
25 ATTTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG 150  
TATCACTGGA GGACTGGGNC CAGGACCTGA CCTGGTGGTA CCAAATCCA 200  
TGAGGCNGNA AT 212

30

## (2) INFORMATION FOR SEQ ID :1102:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG 50  
GTTCGTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT 100  
5 GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC 150  
AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN 200  
GAGTGGAAT TCCANCAT 218

10

(2) INFORMATION FOR SEQ ID :1103:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

GTCAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT 50  
TCGTGTAAGT ACACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG 100  
25 CATTTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA 150  
GTATCACTGG AGGACTGGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC 200  
30 ATGAGCG 207

(2) INFORMATION FOR SEQ ID :1104:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

561

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG 50  
5 ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC 100  
TCTGCCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCCTGAAC 150  
AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT 200  
10 CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN 250  
GTGNAGGCC 259

## 15 (2) INFORMATION FOR SEQ ID :1105:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

ACATGACCCC TTGGACTGAA GCGGCTCAGT AGTAAAGGAG TGTCATGCAG 50  
GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA 100  
30 CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG 150  
CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC 200  
35 ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT 230

## (2) INFORMATION FOR SEQ ID :1106:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

562

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

ACATGNCCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT 50  
CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA 100  
GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG 150  
GTNAGAGGGG GCT 163

15 (2) INFORMATION FOR SEQ ID :1107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA 50  
GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT 100  
GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA 150  
GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT 182

35 (2) INFORMATION FOR SEQ ID :1108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40



563

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1108:

5 CCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTATGC AGGTCAACAC 50  
ATGTGCACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT 100  
TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG 150  
10 AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTGTTT 200  
CGNGCCTTGA AAGA 214

## (2) INFORMATION FOR SEQ ID :1109:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

25

ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTCATGCAG 50  
GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC 100  
30 ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT 133

## (2) INFORMATION FOR SEQ ID :1110:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTCATG 50  
CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA 100  
5 TGCACGGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT 150  
GGAATG 156

## (2) INFORMATION FOR SEQ ID :1111:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1111:

20

GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCCG 50  
AGGTGCCTCA AGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC 100  
25 ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA 150  
AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT 200  
CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT 250  
30 GCATACACCA CGAAATACTA CGAGCCATAA AA 282

## (2) INFORMATION FOR SEQ ID :1112:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

565

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

TAATTAGTTT AACCACTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA 50  
5 ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT 100  
CAAAAGGAAA TAAANNGNCN TGTNAAAGAC CATAACNAT NGTCCATCGG 150  
AGCCCGTATN CACGCAGCTT GTCATAACTA T 181

10

## (2) INFORMATION FOR SEQ ID :1113:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG 50  
25 AACTTAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA 100  
TAGATATATC CAAAAGAAAA TAAATCATTG TTCAAAAAGA CACATACACT 150  
AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA 200  
30 CACTCATGAA TCGGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA 250  
AATACTACGA GCCATAAAG GCGAAATC 278

35

## (2) INFORMATION FOR SEQ ID :1114:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

566

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

ACCTGCAAAC TTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50  
5 TGAGCCATAC AGTTTTTGTT GCAACTAGTC AACTCTCAAC TNACGTGGAC 100  
AGCATGTAAA GAACGAGAGT GACTG 125

## (2) INFORMATION FOR SEQ ID :1115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCGGGGA CCTGCAAAC TTTTGAAAG 50  
ACCAGATAGT AAGTATTTTA TGCTTTGTGA GCCATACAGT TTTTGTGCAA 100  
25 CTAGTCAACT CTCAACTCAC CGTGGACAGC ATGTAAATGG ATGGGAGTGG 150  
CTGCCGG 157

## (2) INFORMATION FOR SEQ ID :1116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAAC TTTTCTGTAA AGACCAGATA GTAAGTATTT TATGCTTTGT 50

567

GAGCCATACA GTTTTGTG CAACTAGTCA ACTCTCAACT NACGTGGACA 100

GCATGTAAAG AACGAGAGTG ACT 123

5 (2) INFORMATION FOR SEQ ID :1117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTGTGTA AAGACCAGAT AGTAAGTATT TTATGCTTG 50

20 TGAGCCATAC AGTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC 100

AGCATGTAAA TGGATGGGAG TGGCT 125

(2) INFORMATION FOR SEQ ID :1118:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

35 ACCTGCAAAC TTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTTT 50

GTGAGCCATA CAGTTTTCGT TGCAACTAGT CAACTCTCAA CTCACCGTG 100

40 GACAGCATGT AAATGGATGG GAGTG 125

(2) INFORMATION FOR SEQ ID :1119:

568

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1119:

10

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT 50

CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT 100

15 CAAAGAGCCA ATGAGAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA 148

## (2) INFORMATION FOR SEQ ID :1120:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

30 AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT 50

AATCAAGAAA AAATAGCACC AACACAATG AGGAGAAAAT GGAAAAAGGG 100

CAGAGTATTT CAAGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT 150

35 TAAGCCTTCA GTTGGCCCTG TAAGCAAACCT GAAGACGTGC AAGTCATCCT 200

TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAACTAG 240

## (2) INFORMATION FOR SEQ ID :1121:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs

569

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG 50  
10 GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA 100  
AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG 150  
15 ATTTTAAAGC CTTACGTCT GCCCTGTAAG CAACTGAAG ACGTGCAAGT 200  
CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGGCA ATGAGAAGGG 250  
ACAG 254

20

(2) INFORMATION FOR SEQ ID :1122:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC 50  
35 NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA 100  
TGAAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA 150  
ACGAATGATT CTTAAGCCTT CACGTTTGCC CTGTAAGCAA ACTGAAGACG 200  
40 TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC 250

570

GAG

253

## (2) INFORMATION FOR SEQ ID :1123:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

15 AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AATGAATCCT 50  
GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAATCCGA GAAAATGGAA 100  
AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT 150  
20 GATTTTAAAG CCTTCACGTC TGCCCTGTAA GCAAACTGAA GACGTGCAAG 200  
TCATCCTTTG 210

## 25 (2) INFORMATION FOR SEQ ID :1124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 231 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC 50  
CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA 100  
40 TGGAAAAAGG GCAGACTATT TAAATGATTA CGGAGACGGG CAAACCAATC 150



571

AACGAATGAT TCTTAAGCCT TCATGTTTGC CCTGTAAGCA AACTGAAGAC 200

GTGCAAGTCA TCCTTTGGAC CCTGGGAGAG T 231

5

(2) INFORMATION FOR SEQ ID :1125:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

AAGTCCCATC AGCAACCCGT TTTTACCAG ATGTCCTCA AGAATGCGCC 50

20 CGTGGCCCTC CAGTTCCTGC GCACTAAGAG CGTCCCGCT 89

(2) INFORMATION FOR SEQ ID :1126:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA 50

35

ACCAAAACTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC 100

ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT 150

40 ATGCTACTGG ACACATGCCC ACACAATAAT ANTCANRTGT NTYGTAGGC 200

CTACT 205

572

## (2) INFORMATION FOR SEQ ID :1127:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

GCAAGGCCTG GCCGACAACA CCCTTATTGC TAAAGTAAAT AATGNCGCGC 50  
15 GGGGCCTGGA CCACCCTCTG GAAGAAGATT GTACCTTGGA GCTTCTCAAG 100  
TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA 150  
A 151

20

## (2) INFORMATION FOR SEQ ID :1128:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

GAGCACCCCA GCCCATAACA CAGAACTCGT CCCCTACCC CCCTCAGCAA 50  
35 GCCGGAGAGG CTAGCCCAAG TAATCATAAY AACAGCCGCC CGAGAGCAGC 100  
CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT 150  
GACAGACGAG ACCTGCCAGG ACGCAGCCAT TCGGGGCTGC AAGGCCTCRC 200  
40 CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT 237

573

## (2) INFORMATION FOR SEQ ID :1129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

GCCTCGTGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG 50  
CACCACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT 100  
CCTTAAGATC ATCCAACATAT AGGATG 126

## (2) INFORMATION FOR SEQ ID :1130:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

30

GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG 50  
AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT 100  
CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG 150  
TTTATTTGCA AGGATTTTTC TTTCGRGGGC GGAGGGGAGA GAAAAGTAAA 200  
TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCTT YGTATC 246

40

## (2) INFORMATION FOR SEQ ID :1131:

574

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1131:

10

CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA 50  
TCCTCTGTCT GACCATGATT TTTTCCCTCA AATACAACCA CTCCTCGACT 100  
TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAG CTCTTGCACT 150  
GTACACTTAG AAGTGACAA TTAAAGCATT ATAGAGCTAT CTACACACCG 200  
ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG 250  
TGCAGACAGA ACTAAAACCA ACT 273

20

## (2) INFORMATION FOR SEQ ID :1132:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35

GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG 50  
TG GTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC 100  
CTTAGACATT CTTCCAGGCA GGATCAAACCT CAAAGGAAAA GGAATTTGTG 150  
AAGCAAACCA TGGCTTTGTC ACAGTAAAGT AATTGTCACT CTCAACCCAG 200

40

575

AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA 250

AGCCAATGTA TCTGACCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT 300

5 ATTTCTGTTT GTTAAAAAGT TCAGAATTT 329

(2) INFORMATION FOR SEQ ID :1133:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

CCCCGAGCTA GTTGTCCTGA CCTG 24

20

(2) INFORMATION FOR SEQ ID :1134:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 297 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

GAGGATCCAC AAACCATGGA AACTCTCGC GGCTGCCACT CCCCCATGAC 50

35 CACCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA 100

TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG 150

CGGCCCCCTGC CGGGCACCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT 200

40

CCAGGAATCT CTACCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA 250

576

CCAAACCTCG CCAGAAGGCT TCTTTTCGGG TTGATCGCCA TCTATTY

297

(2) INFORMATION FOR SEQ ID :1135:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15 GCCGCTTAC TGCTCAGTTC GGAGCTACCG CTTGAAAGC AACAAAAAG 50

CNTTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA 93

(2) INFORMATION FOR SEQ ID :1136:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:

30

CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG 50

TTGTGGGAGA TAACGGTGGC ATAGTTCCCT GATGCCCCGG CCAGCTTGCC 100

35 ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA 150

TGGTGCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG 200

CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC 250

40

CGCCCGCTTC TTAAACCAAG ACAGATCCCG GAAGGCCGCC TGGGCAAGGG 300

577

GCCCCCTCRAA CCCGGGGCTA TACACGTCAA AATC

334

(2) INFORMATION FOR SEQ ID :1137:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15 CGAGGATCCG CATACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG 50  
ATGAAGAAAC TCCAAACCCT TTGACAGCTC CTCGGGGTNA AACCTGGNAY 100  
AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT 150  
20 CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT 199

(2) INFORMATION FOR SEQ ID :1138:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35 CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCAGCGC CGCTCCGCGT 50  
GGCACCCGGC TCGCTCCGAG TTTCAGGCTC GTGCTAAGCT AGCGCCGTCG 100  
TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC 150  
40 ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG 200

578

TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT 250  
TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG 300  
5 AAGG 304

## (2) INFORMATION FOR SEQ ID :1139:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 277 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

20 GAGGATCCGG GTACCATGAG AAACCTTTGAA GCCAGAGATT TTAAACAATC 50  
AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAACAAA 100  
CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC 150  
25 CTTTAATAGT TATCTAAATG CAGAGTTTGT TTATGAAATG AACCAAAGCA 200  
GTTTGTTCATT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC 250  
CACTACTGGC TAAAGAAACT AAGTAAA 277

30

## (2) INFORMATION FOR SEQ ID :1140:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1140:



579

CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCCAA 50  
AAGAGAGCTC CCTGAGAAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT 100  
5 TTTAGCAGAG CAAATTTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG 150  
GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAAGTCA GACTGGGCTC 200  
CAGCTTCT 208

10

(2) INFORMATION FOR SEQ ID :1141:

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

25

CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG 50  
CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG 100  
TCAACAATGG TTAACCTTCAG CCGTACATTG CTTTCTGAA GCTCATAACT 150  
TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACTTT 200  
30 TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT 250  
GTCTCACCAA TACAAAGGAT GTTG 274

35

(2) INFORMATION FOR SEQ ID :1142:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

580

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1142:

GCCTGCACAT TGA CTGTGGG AACTCGGAA ACAAGCTCAC ATCTCCCCGT 50  
5 GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAAGT CAGTTGCCAC 100  
CTTCCTCTAT GCGGAGGTCT TTGTGTGTT GCTTCTCTGC ATTCCCTTCA 150  
10 TTTCTCCTAA AAGATGGCAG AAGATTTTAA AGTCCCGGCT GATGGAGTTG 200  
TTAGTGTCTT ATGGTAACAC CTTCTT 226

## (2) INFORMATION FOR SEQ ID :1143:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

25

RGGRTCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC 50  
TGRRCRGNTG NCNGTGAGGR CRTGNRGGNC CRTGCGAGTG GGCTTACCGN 100  
30 TAGGTTCTGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG 150  
GNANGRTGNN GTGGAGRG 168

## (2) INFORMATION FOR SEQ ID :1144:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

581

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT 50  
5 TCTTGAGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTTGC 100  
CAGGATTTGA GGAAATCGAC TGCCTTCACT CTCCTGAA ACTTTGAAGT 150  
CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT 200  
10 AAACAACCTT ATAGTGTTTT CGCTTGAAT TGTATGAATT CTTAGAAGT 250  
AGAAGT 256

## 15 (2) INFORMATION FOR SEQ ID :1145:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

AAACACAAGG CTAAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA 50  
GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG 100  
30 TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT 150  
GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG 184

## 35 (2) INFORMATION FOR SEQ ID :1146:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

582

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

5 CGAGGATCCG GGTACCATGG CCCAAGAGT GAATGATGTA TCCCAGGGCG 50  
CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG 100  
ATTTCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT 150  
10 TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG 200  
GTGCTGAGAA GAATGCACAA G 221

## (2) INFORMATION FOR SEQ ID :1147:

15

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

25

CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT 50  
TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT 100  
30 TAAGGATTCT CACATTCAGG ACAGAGAACA AATTTTTTAA TGAATCCATC 150  
CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC 200  
RRTMATCTT AACANCAAAC NGMGMTGNN NTCCCRNCTT ATAACCMAAA 250  
35 GATNT 255

## (2) INFORMATION FOR SEQ ID :1148:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid

583

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:

	CGAGGATCCA GGTACCATGG ACGATTCACA GCCCCTGGCC ACTGGCCATT	50
10	TCCAGTGGTA GGGAGCACAC TGRTCACATT CGAGACCCAC CACGTTGAGC	100
	AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC	150
	CCCAGGATGT TGTAAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG	200
15	AGTCGGTGAC GCCCGATTG GATCGGGTGT	230

(2) INFORMATION FOR SEQ ID :1149:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

30	GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA	50
	GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTGAGACG TTCTCCTTTC	100
	AGGCAGAAAT CGCCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG	150
35	AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT	200
	GGACAAAATT CGATATAAAA GCT	223

40

(2) INFORMATION FOR SEQ ID :1150:

(i) SEQUENCE CHARACTERISTICS:

584

- (A) LENGTH: 272 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1150:

10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC	50
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGATTC CTAATGCCCT	100
	ATGATCACGT GGAACATAACA TCAATGACA TGAAGAACGT GCCAGAAGCC	150
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	200
	CTTTATGTCC AAGAACAAGG ATGCGATGGG TATTTCGTGA NGCTATTTGA	250
20	NMTRAGGRMA GNCTGNAAGG TM	272

(2) INFORMATION FOR SEQ ID :1151:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 140 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1151:

35	TGAGGATTTA TAGATTANAG CTAGAGTTCA CATTTTATGG ATTACAACCA	50
	AAAAAACCT GAAAAAGAAA AAAACAAAAA AAGCTCAAAA GCAATCACAA	100
	GGATAGTTGA ATCCCTCTTT AAACCCCAAA AGCAACCCCC	140

40 (2) INFORMATION FOR SEQ ID :1152:

(i) SEQUENCE CHARACTERISTICS:

585

- (A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1152:

10	AAGGATCCGG GTACCATGTA TTCCCCGGT ATCAGCAGAG GCGGTACGG	50
	GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG	100
	GTCACCAAGG TAGATTTCCTA GCAGCCTAGT CCAGCTGAAC GCTTCCAGC	150
15	CTTGCTTTTT AGCAGCTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC	200
	TTTCATTG	208

## 20 (2) INFORMATION FOR SEQ ID :1153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1153:

	CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCTGGA	50
	TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG	100
35	CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACTCCAG	150
	GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG	200
40	GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA	250
	GAMGCCNMAC AGGGCTRGGG ACTG	274

586

## (2) INFORMATION FOR SEQ ID :1154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1154:

GAGGATCCAC CGACCATGGA ACACTCTCAA TGGCTGCAAC CACCCCGTGG 50  
CCCCCTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA 100  
CCAACAGCTG CAGCCCCTGA GATCTTCACC TTAGACCCTC TCCCGAAGCC 150  
CGCAGCCGCC CCTGCGAACC CTCCAACCTG TTCACACGCG CCGAAAGCCT 200  
ATTCCCAGGA CTCTCTGCCC CTACGTGACC GNCCCTAGCT GCTAGTCGAG 250  
AATCCGAACT CCGCTCC 267

25

## (2) INFORMATION FOR SEQ ID :1155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

CTCAAACCCC GNTTCCCCC TAATAAGAGC AACTAAAAA CTTCTGATAA 50  
CCACAATAAA AGCGTGCAAT TGAGCACAAT TCAAAAGCCA ACCCCTTCGA 100  
AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG 150

40



587

CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC 200

CGTCTANCAA GGCAACGGCC GCCTTTGAAT T 231

5 (2) INFORMATION FOR SEQ ID :1156:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCCA TCCACACCTG 50

20 CCGCCAGCTC ACCGTGTATG ATGATATCAC CNCGCTCGCC ACCAACRACG 100

GCTCYAACMT GTGCAAGGCC GCCTTCAA 128

(2) INFORMATION FOR SEQ ID :1157:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

35 GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCC GGCTCT 50

GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCCACA AGGGCAGAAA 100

GGTGAGCCTT ATGCACTGCC TAAAGA 126

40

(2) INFORMATION FOR SEQ ID :1158:

588

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

10

AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA 50

CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT 100

15

T 101

## (2) INFORMATION FOR SEQ ID :1159:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG 50

30

GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC 100

CCCACACACG GTGGCGGTGC GGGTGAAGTGA GAAGGGGAGG TCGAAGGTGC 150

35

CATCTTCTTC AGGCCCTCC AC 172

## (2) INFORMATION FOR SEQ ID :1160:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

589

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA 50  
TGGTTATTTT CCAGGACCAC ACGATTGCCC TACGTCCTG GAAGGCTATG 100  
TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG 150  
CTTTGACCCT GTGATGCCAT TTTAATCAAC CCTGCTTGGT TTTAGAGGAT 200  
TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT 235

## (2) INFORMATION FOR SEQ ID :1161:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 284 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG 50  
TTAGATACAA ATGCAAAACG CTCCTAAAA AACGGCCTGA AAAAAAATC 100  
ACAGACAATG CCAAACCTTA TAGGTCTGTA TTTTCCTTA TACAAAATGC 150  
CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG 200  
ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA 250  
ACCCTCATAA AGCCTTAAAA GTACATTTGT GAAA 284

40

## (2) INFORMATION FOR SEQ ID :1162:

590

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

10

GCTCACATAA ATTTCTTCAC CGACCCTTTT CCTTCCAGCT TCCTTACTAT 50

AAAAAACCCC ACA TATA TGTTTCATCAT CATCCATACT AACCAACCCC 100

15

GTCACCATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAAACCTTG 150

TTACCACCTC TAGGGGCAGA CCCCTTTTCA GATATATTCA AGAGTTTAAT 200

ATCCTCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA 250

20

ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC 287

## (2) INFORMATION FOR SEQ ID :1163:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

35

GAGGATCCAA AAACCATAAA ATTCATCATC CCCAGCAGGT GCNCTAGCTA 50

TACTTTATTA CAGCAAARCA CAACCACACG CTGAMCTANM TCGTATAGAT 100

AAACACCAAT CATGGGTCGG CC 122

40

## (2) INFORMATION FOR SEQ ID :1164:

591

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1164:

10

GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG 50

GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCCTCTC CACTTGCAAC 100

15

CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTCTGAAGC CT 142

## (2) INFORMATION FOR SEQ ID :1165:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

30

TATCCCCCG GTATCAGCAG AGGCGTGAC GGGCACTGCT TTAAACTGG 50

GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC 100

CAGCAGCCCT AGTCCAGCTG AACACTTCC AGCCTTGCTT TTCAGCAGCT 150

35

TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG 200

GATGAGAATA GAGAACTCA 219

## (2) INFORMATION FOR SEQ ID :1166:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs

592

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:

10 GAGGATCCAC CAACCATAGA AAGGAAACAA CACTGGAGT GAACCCGACC 50  
CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAC 100  
AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGTTTNT CAATCCAAAC 150  
15 ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC 200  
AA 202

20

(2) INFORMATION FOR SEQ ID :1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:

GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAATG ACCTTTACGA 50  
AGACACGTCT GATACCCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG 100  
35 GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC 150  
ATCTGGAGA 159

40

(2) INFORMATION FOR SEQ ID :1168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs

593

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1168:

10 CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG 50  
CGATTGCCAC CGCTTCTCTC TAGTCTCAG AGGGGTTTCC CGCCTCGCAC 100  
CCCCACCTCT GGACTTGCCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC 150  
15 CAGCGCTTAG GTCGGAGCGA GCCTGGGGCC ACCGCCGTGA AGACATCGCG 200  
GGGACCGATT C 211

20

## (2) INFORMATION FOR SEQ ID :1169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1169:

GGATTTCCGG TCCTGGCTTT CTGATATTC TAAAATCGAC CTGGAATCAA 50  
CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC 100  
35 CATGATGATG AGCTGGAAGG GCGCCGATT GCCTTCATCC TGTACCTGGT 150  
TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG 200  
ATGAACACTT T 211

40

## (2) INFORMATION FOR SEQ ID :1170:

594

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10

GAGGATCCGC GCAACCATAG AACTCACAAC CCAGCCATAT ACCTCAGACA 50  
CAATGGAATG GCGCGAGGTC GAGGTNGACA AACCCCTGAGT AATGTTGGGC 100  
ACTTCCGCAC CGGAGCTGTT CTTACCTTGG ATAAAGTGGG TGTTATTGCT 150  
ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC 200  
CTATCCACCA ACGNCGAACA ATATGCTGTT GCCAMGATTG AGCACGAGCC 250  
GTTTGGGCTC AACGGC 266

20

## (2) INFORMATION FOR SEQ ID :1171:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35

GGCACAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG 50  
CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG 100  
GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTTGAGGGC 150  
TTTAATCCTT TAAAACT 167

40



595

## (2) INFORMATION FOR SEQ ID :1172:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC 50  
15 TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG 100  
ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT 150  
TACTGAGGAT ACGCAACTCA TAAAACTCTA CTTAAAGCAA CAGGGCAGAC 200  
20 GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC 232

## (2) INFORMATION FOR SEQ ID :1173:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

35 GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT 50  
CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC 93

## (2) INFORMATION FOR SEQ ID :1174:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs

596

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

GCCTTTTTTT	ACCCGCCGGA	AGCTACAGCT	TTTGCCCCCC	CAAAAAACC	50
CCACCCTTTT	ACCCACCGCG	GACCCAAAAA	CAGCAAAAC	CAAGGACCTC	100
TCCCAACCCC	AACCCCTCCT	TTTTGGCCCT	TCCTTCCCCC	CCTCCCAGCC	150
CACCCCCAGA	CACCTCAATC	CCCCAAAAGG	ATGCCCTAAA	CCTCTCCTAA	200

## (2) INFORMATION FOR SEQ ID :1175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

GAGGATCCAA	AAACCATGGC	ATTCATCAGC	CCCAGCAGGT	GTCCCAGCCA	50
TGACTTACCA	TAGCAAAACA	CAACCACACA	CTAACCTGCA	TGCCTAGCT	100
TACTGATGAT	GATGTCCTGG	T			121

## (2) INFORMATION FOR SEQ ID :1176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC

26

5

(2) INFORMATION FOR SEQ ID :1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG

50

20

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT

100

CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT

150

TCAGGATGGA TTMAAGNAMG CAGAGAGG

178

25

(2) INFORMATION FOR SEQ ID :1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA

50

40

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCCACAG TTGCCCCGTG

100

TGTTATGCAT CAGTTATACA GGTATCCCAC CAAGTTCAAG TCAA

144

598

## (2) INFORMATION FOR SEQ ID :1179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

	GACCAGGGAG GAGGTTTAAT CAACTTGGAC CCCCTCCGGC CTAGCCGCCG	50
15	AGGAGGTGCA TTCGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG	100
	TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCAGCTT TTGATTACT	150
	GATCTCGCTG AAAAGACAGA CGCTTTTAGA TACCGAGTCG ATAGGGGGTC	200
20	TGCGGTACTT TTCAGTAGAT AGGTGGTGCT TGT	233

## (2) INFORMATION FOR SEQ ID :1180:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

35	CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC	50
	CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA	100
	TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCGCCC GAGCCCCCTT	150
40	CTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG	200

599

AGGTAGACGG GACCAAGATC TGCTG

225

(2) INFORMATION FOR SEQ ID :1181:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15 TGAGGATTTA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC 50  
GATGAATAAG CTTGATGTGG CCTAGTTTTN NGNNNNNTGG NYATGGTNNA 100  
TCNNNTTANT TTTTGGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG 150  
20 TTTAGAGTTT GGAAGCGGCN RNGCGTARMG NNACTCYACG CTCGCNNCTN 200  
TTGNNNNACA GMRGGNTCTC TNGGRTGAGT GGRINCMTT GGMGGNNTCN 250  
25 NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTNGGCTN GCT 293

(2) INFORMATION FOR SEQ ID :1182:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

40 GAGGATCCGG GTACCATGGC TCTCTCTTC TTTTTTTCT TTTTCTGGC 50  
GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA 100

600

CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTTCTCA 150  
GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCATTCC 200  
5 TTCTGGCTGT TGAGACCCCG TGGACTCCCC TGGATTCCAG AGNNTNATTT 250  
NG 252

## (2) INFORMATION FOR SEQ ID :1183:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

20

ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG 50  
AAACTGTAGA TTCGGCTTAA GGAATAGTC ATTTATAGAC TATTCAATAG 100  
25 AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT 150  
ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT 200  
GT 202

30

## (2) INFORMATION FOR SEQ ID :1184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTTCGTGG TTCACAATTT CTCAGTCTC TTA

43

(2) INFORMATION FOR SEQ ID :1185:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

15 ACCGTCCTTC TGGTTCATCC TAGCAAAAAT CTCACCATCT TCTATCAC

48

(2) INFORMATION FOR SEQ ID :1186:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

ACATCATCCG AGTCCCCTCT ACAGTGTTC TGTGATCGT TGCATCCCCC 50

30 TGGTTTGGA AATAAATATA AACTGCCCCG CAAGAGATAA AATTGTATTT 100

TTTA 104

35 (2) INFORMATION FOR SEQ ID :1187:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 40

602

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG 50  
5  
AGAATCCTAT TCAGTGCTCC CTTAGA 76

## (2) INFORMATION FOR SEQ ID :1188:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

20 AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA 42

## (2) INFORMATION FOR SEQ ID :1189:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

GGCGGACGTG CGCGCCTTGT CTTGCGGGCA CCTGGGCCTG AGGTGCGTGC 50  
35 CTCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC 100  
GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC 150  
40 GCCAAGGCCT TTTATTTATG GCTAGTTTGC TCTCGTGAAA TACTAACATC 200  
GTTTAAATGG CACTCATCAA GTACGCAAAT GATATGATTT AACCTCGCGC 250



603

AAT

253

## (2) INFORMATION FOR SEQ ID :1190:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15	GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG	50
	TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA	100
	CAACTACTCC AATTGCCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT	150
20	GAATTTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAAGGCTC	200
	AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT	250
25	TT	252

## (2) INFORMATION FOR SEQ ID :1191:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

40	GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCCAAC GATCTAACTA	50
	ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC	100

604

TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TGCCAACCA 150

CCCTTCCGGC TGCCCTTGTG TTGACTTG 178

5 (2) INFORMATION FOR SEQ ID :1192:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCGG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT 50

CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT 100

20 GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNG 150

NGGGCA 156

25 (2) INFORMATION FOR SEQ ID :1193:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTGT AATACAGACA 50

40 TAACTGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA 99

605

## (2) INFORMATION FOR SEQ ID NO: 1194

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

NNNNTCCTTC TCCTGCGACA GACA

24

15

## (2) INFORMATION FOR SEQ ID NO: 1195

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

TGTCTGTCGC AGGAGAAGGA

20

30

## (2) INFORMATION FOR SEQ ID NO: 1196

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:

AANNCTCGG ACAGTGCTCC GAGAAC

26

606

## (2) INFORMATION FOR SEQ ID NO: 1197

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNTCTCGG ACAGTGCTCC GAGAAC

26

15

## (2) INFORMATION FOR SEQ ID NO: 1198

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA

22

30

## (2) INFORMATION FOR SEQ ID NO: 1199

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

GTTCTCGGAG CACTGTCCGA GAG

23

607

## (2) INFORMATION FOR SEQ ID NO: 1200

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC

23

15

## (2) INFORMATION FOR SEQ ID NO: 1201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGTCTGTCG CAGGAGAAGG AA

22

30

## (2) INFORMATION FOR SEQ ID NO: 1202

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:

CTGTCTGTCG CAGGAGAAGG AG

22

608

## (2) INFORMATION FOR SEQ ID NO: 1203

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG

17

15

## (2) INFORMATION FOR SEQ ID NO: 1204

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCG

24

30

## (2) INFORMATION FOR SEQ ID NO: 1205

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:

GATCCGGCTC GAGT

14

609

## (2) INFORMATION FOR SEQ ID NO: 1206

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCG

18

15

## (2) INFORMATION FOR SEQ ID NO: 1207

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAAACGAC GGCCAGT

17

30

## (2) INFORMATION FOR SEQ ID NO: 1208

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:

CGAGGTCGAC GGTATCG

17

610

## (2) INFORMATION FOR SEQ ID NO: 1209

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG

17

15

## (2) INFORMATION FOR SEQ ID NO: 1210

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTTCGAC AAGCTTGAAT TCGCGGCCGC TTTT TTTT TTTT

50

TTTTT

56

30

## (2) INFORMATION FOR SEQ ID NO: 1211

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:



611

GCCWSCGCCG A

11

(2) INFORMATION FOR SEQ ID NO: 1212

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

15 GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO: 1213

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

30 TTGACACCAG ACCAACTGGT AATG

24

35 In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

40 85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,  
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,  
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

5

10

15

## CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-
  - (a) a sequence selected from SEQ ID Nos 1 to 1193;
  - (b) an allelic variation of a sequence as defined in (a); or
  - (c) a sequence complementary to (a) or (b).
2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.
3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.
4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.
5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.
6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.
7. A nucleic acid sequence as claimed in claim 2 or claim 3 and encoding at least a portion of a biologically active polypeptide.
8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.
9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.
10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a gene.
12. A DNA fragment comprising a gene obtainable by the use defined in claim 11.
13. An expression vector comprising a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a DNA fragment as claimed in claim 12, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.
14. A vector as claimed in claim 13, wherein said vector control or regulatory sequence comprises a regulatable promoter.
15. Host cells which incorporate as a heterologous part of their expressible genetic information a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, or a DNA fragment as defined in claim 12.
16. A process for the production of a polypeptide comprising cultivating host cells as defined in claim 15.
17. An antibody directed against a polypeptide obtainable by the performance of a process as defined in claim 16.
18. An antibody as claimed in claim 17 and which is monoclonal.
19. A novel gene product or portion thereof encoded by a fragment as defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as defined in any one of claims 2, 3 or 7, or encoded by the gene comprised in a DNA fragment as defined in claim 12.

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>5</sup> :</b> C12N 15/11, 15/62 C12P 21/08, C07K 15/28 C12Q 1/68	<b>A3</b>	<b>(11) International Publication Number:</b> WO 94/01548 <b>(43) International Publication Date:</b> 20 January 1994 (20.01.94)
<b>(21) International Application Number:</b> PCT/GB93/01467 <b>(22) International Filing Date:</b> 13 July 1993 (13.07.93) <b>(30) Priority data:</b> 9214857.6 13 July 1992 (13.07.92) GB <b>(71) Applicant (for all designated States except US):</b> MEDICAL RESEARCH COUNCIL [GB/GB]; 20 Park Crescent, London W1N 4AL (GB). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only) :</b> SIBSON, David, Ross [GB/GB]; 37 Grimsdells Lane, Amersham, Buckinghamshire HP6 6HF (GB). GROSS, Jacqueline [GB/GB]; 47 Boxmoor Road, Kenton, Middlesex HA3 8LH (GB). HADFIELD, Kathryn, Mary [GB/GB]; 5 Carlisle Terrace, St Ives, Huntingdon, Cambridgeshire PE17 4PQ (GB). HOWELLS, David [GB/GB]; 77 Puttocks Drive, Welham Green, Hatfield, Hertfordshire AL9 7LW (GB). STARKEY, Michael [GB/GB]; 27 Creasy Close, Abbots Langley, Hertfordshire WO5 0HS (GB). KELLY, Maria [IE/GB]; 24A Oxford Road, Ealing, London W5 3ST (GB). SHAW, Diana [GB/CA]; 342 Glacier Hall, University of Calgary, 2500 University Drive NW, Calgary, Alberta T2N 1N4 (CA).		<b>(74) Agent:</b> BIZLEY, Richard, Edward; Hepworth Lawrence Bryer & Bizley, 2nd Floor Gate House South, West Gate, Harlow, Essex CM20 1JN (GB). <b>(81) Designated States:</b> AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> <b>(88) Date of publication of the international search report:</b> 31 March 1994 (31.03.94)
<b>(54) Title:</b> HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW  <b>(57) Abstract</b> <p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>		

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# INTERNATIONAL SEARCH REPORT

International Application No. PCT/GB 93/01467

<b>I. CLASSIFICATION OF SUBJECT MATTER</b> (If several classification symbols apply, indicate all) <sup>6</sup>		
According to International Patent Classification (IPC) or to both National Classification and IPC: Int.C1.5      C 12 N 15/11      C 12 N 15/62      C 12 P 21/08 C 07 K 15/28      C 12 Q 1/68		
<b>II. FIELDS SEARCHED</b>		
Minimum Documentation Searched <sup>7</sup>		
Classification System	Classification Symbols	
Int.C1.5	C 12 N      C 12 Q      C 07 K	
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched <sup>8</sup>		
<b>III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup></b>		
Category <sup>10</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
Y	SCIENCE vol. 252, 21 June 1991, LANCASTER, PA US pages 1651 - 1656 ADAMS, M. ET AL. 'Complementary DNA sequencing: expressed sequence tags and human genome project' see the whole document ---	1-19
Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA vol. 88, March 1991, WASHINGTON US pages 1943 - 1947 PATANJALI, S. ET AL. 'Construction of a uniform-abundance (normalized) cDNA library' cited in the application see the whole document ---      -/-	1-19
<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p><sup>10</sup> Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&amp;" document member of the same patent family</p> </div> </div>		
<b>IV. CERTIFICATION</b>		
Date of the Actual Completion of the International Search		Date of Mailing of this International Search Report
08-10-1993		01.03.94
International Searching Authority		Signature of Authorized Officer
EUROPEAN PATENT OFFICE		ANDRES S.M.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
Y	NUCLEIC ACIDS RESEARCH vol. 18, no. 19, 11 October 1990, ARLINGTON, VIRGINIA US pages 5705 - 5711 KO, M.S.H. 'An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs' cited in the application see the whole document ---	1-19
Y	NATURE vol. 355, 13 February 1992, LONDON GB pages 632 - 634 ADAMS, M. ET AL. 'Sequence identification of 2,375 human brain genes' see the whole document ---	1-19
Y	GENE vol. 81, 1989, AMSTERDAM NL pages 295 - 306 AKOWITZ, A. & MANUELIDIS, L. 'A novel cDNA/PCR strategy for efficient cloning of small amounts of undefined RNA' see the whole document ---	1-19
P,Y	WO,A,9302214 (MEDICAL RESEARCH COUNCIL) 4 February 1993 see the whole document -----	1-19



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International application No.

PCT/GB93/01467

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos. because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos. because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos. because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.2(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see PCT/ISA/206 mailed on 29.11.93

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-19(all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

GB 9301467  
SA 76316

The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

**FD FORM P0479**

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82